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(54) Title: COMPOSITIONS ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE

(57) Abstract: Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.



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COMPOSITIONS ISOLATED FROM SKIN CELLS  
AND METHODS FOR THEIR USE

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Technical Field of the Invention

This invention relates to polynucleotides, polypeptides, polypeptides expressed in skin cells, and various methods for treating a patient involving administration of a polypeptide or polynucleotide of the present invention.

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Background of the Invention

The skin is the largest organ in the body and serves as a protective cover. The loss of skin, as occurs in a badly burned person, may lead to death owing to the absence of a barrier against infection by external microbial organisms, as well as loss of body temperature and body fluids.

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Skin tissue is composed of several layers. The outermost layer is the epidermis which is supported by a basement membrane and overlies the dermis. Beneath the dermis is loose connective tissue and fascia which cover muscles or bony tissue. The skin is a self-renewing tissue in that cells are constantly being formed and shed. The deepest cells of the epidermis are the basal cells, which are enriched in cells capable of replication. Such replicating cells are called progenitor or stem cells. Replicating cells in turn give rise to daughter cells called 'transit amplifying cells'. These cells undergo differentiation and maturation into keratinocytes (mature skin cells) as they move from the basal layer to the more superficial layers of the epidermis. In the process, keratinocytes become cornified and are ultimately shed from the skin surface. Other cells in the epidermis include melanocytes which synthesize melanin, the pigment responsible for protection against sunlight. The Langerhans cell also resides in the epidermis and functions as a cell which processes foreign proteins for presentation to the immune system.

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The dermis contains nerves, blood and lymphatic vessels, fibrous and fatty tissue. Within the dermis are fibroblasts, macrophages and mast cells. Both the epidermis and dermis are penetrated by sweat, or sebaceous glands and hair follicles. Each strand of hair is derived from a hair follicle. When hair is plucked out, the hair re-grows from epithelial cells directed by the dermal papillae of the hair follicle.

When the skin surface is breached, for example in a wound, the stem cells proliferate and daughter keratinocytes migrate across the wound to reseal the tissues. The skin cells therefore possess genes activated in response to trauma. The products of these genes include several growth factors, such as epidermal growth factor, which mediate the proliferation of skin cells. The genes that are activated in the skin, and the protein products of such genes, may be developed as agents for the treatment of skin wounds. Additional growth factors derived from skin cells may also influence growth of other cell types. As skin cancers are a disorder of the growth of skin cells, proteins derived from skin that regulate cellular growth may be developed as agents for the treatment of skin cancers. Skin derived proteins that regulate the production of melanin may be useful as agents, which protect skin against unwanted effects of sunlight.

Keratinocytes are known to secrete cytokines and express various cell surface proteins. Cytokines and cell surface molecules are proteins, which play an important role in the inflammatory response against infection, and also in autoimmune diseases affecting the skin. Genes and their protein products that are expressed by skin cells may thus be developed into agents for the treatment of inflammatory disorders affecting the skin.

Hair is an important part of a person's individuality. Disorders of the skin may lead to hair loss. Alopecia areata is a disease characterized by the patchy loss of hair over the scalp. Total baldness is a side effect of drug treatment for cancer. The growth and development of hair is mediated by the effects of genes expressed in skin and dermal papillae. Such genes and their protein products may be usefully developed into agents for the treatment of disorders of the hair follicle.

New treatments are required to hasten the healing of skin wounds, to prevent the loss of hair, enhance the re-growth of hair or removal of hair, and to treat autoimmune

and inflammatory skin diseases more effectively and without adverse effects. More effective treatments of skin cancers are also required. There thus remains a need in the art for the identification and isolation of genes encoding proteins expressed in the skin, for use in the development of therapeutic agents for the treatment of disorders including those associated with skin.

#### Summary of the Invention

The present invention provides polypeptides and functional portions of polypeptides, which may be expressed in skin cells, together with polynucleotides encoding such polypeptides or functional portions thereof, expression vectors and host cells comprising such polynucleotides, and methods for their use.

In specific embodiments, isolated polynucleotides are provided that comprise a polynucleotide selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (b) complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (e) sequences having a 99% probability of being the same as a sequence of (a)-(d); and (f) sequences having at least 50%, 75%, 90% or 95% identity to a sequence of (a)-(d).

In further embodiments, the present invention provides isolated polypeptides comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, together with isolated polynucleotides encoding such polypeptides. Isolated polypeptides which

comprise at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725; and (b) sequences having 50%, 75% or 90% identity to a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, are also provided.

In related embodiments, the present invention provides expression vectors comprising the above polynucleotides, together with host cells transformed with such vectors.

In a further aspect, the present invention provides a method of stimulating keratinocyte growth and motility, inhibiting the growth of epithelial-derived cancer cells, inhibiting angiogenesis and vascularization of tumors, or modulating the growth of blood vessels in a subject, comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398.

Methods for modulating skin inflammation in a subject are also provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 338 and 347; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 338 and 347. In an additional aspect, the present invention provides methods for stimulating the growth of epithelial cells in a subject. Such methods comprise administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 129 and 348; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 129 and 348.

In yet a further aspect, methods for inhibiting the binding of HIV-1 to leukocytes, for the treatment of an inflammatory disease or for the treatment of cancer in a subject are provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group  
5 consisting of: (a) sequences provided in SEQ ID NOS: 340, 344, 345 and 346; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 340, 344, 345 and 346.

As detailed below, the isolated polynucleotides and polypeptides of the present invention may be usefully employed in the preparation of therapeutic agents for the  
10 treatment of skin disorders.

The above-mentioned and additional features of the present invention, together with the manner of obtaining them, will be best understood by reference to the following more detailed description. All references disclosed herein are incorporated herein by reference in their entirety as if each was incorporated individually.

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#### Brief Description of the Drawings

Fig. 1 shows the results of a Northern analysis of the distribution of huTR1 mRNA in human tissues. Key: He, Heart; Br, Brain; Pl, Placenta; Lu, Lung; Li, Liver; SM, Skeletal muscle; Ki, Kidney; Sp, Spleen; Th, Thymus; Pr, Prostate; Ov, Ovary.

20 Fig. 2 shows the results of a MAP kinase assay of muTR1a and huTR1a. MuTR1a (500ng/ml), huTR1a (100ng/ml) or LPS (3pg/ml) were added as described in the text.

Fig. 3 shows the stimulation of growth of neonatal foreskin keratinocytes by muTR1a.

25 Fig. 4 shows the stimulation of growth of the transformed human keratinocyte cell line HaCaT by muTR1a and huTR1a.

Fig. 5 shows the inhibition of growth of the human epidermal carcinoma cell line A431 by muTR1a and huTR1a.

Fig. 6 shows the inhibition of IL-2 induced growth of concanavalin A-stimulated

murine splenocytes by KS2a.

Fig. 7 shows the stimulation of growth of rat intestinal epithelial cells (IEC-18) by a combination of KS3a plus apo-transferrin.

Fig. 8 illustrates the oxidative burst effect of TR-1 (100 ng/ml), muKS1  
5 (100 ng/ml), SDF1 $\alpha$  (100 ng/ml), and fMLP (10  $\mu$ M) on human PBMC.

Figure 9 shows the chemotactic effect of muKS1 and SDF-1 $\alpha$  on THP-1 cells.

Figure 10 shows the induction of cellular infiltrate in C3H/HeJ mice after intraperitoneal injections with muKS1 (50  $\mu$ g), GV14B (50  $\mu$ g) and PBS.

Figure 11 demonstrates the induction of phosphorylation of ERK1 and ERK2 in  
10 CV1/EBNA and HeLa cell lines by huTR1a.

Figure 12 shows the huTR1 mRNA expression in HeLa cells after stimulation by muTR1, huTR1, huTGF $\alpha$  and PBS (100 ng/ml each).

Figure 13 shows activation of the SRE by muTR1a in PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells.

15 Figure 14 shows the inhibition of huTR1a mediated growth on HaCaT cells by an antibody to the EGF receptor.

Figure 15A shows the nucleotide sequence of KS1 cDNA (SEQ ID NO: 464) along with the deduced amino acid sequence (SEQ ID NO: 465) using single letter code. The 5' UTR is indicated by negative numbers. The underlined NH<sub>2</sub>-terminal amino acids  
20 represent the predicted leader sequence and the stop codon is denoted by \*\*\*. The polyadenylation signal is marked by a double underline. Figure 15B shows a comparison of the complete open reading frame of KS1 (referred to in Fig. 15B as KLF-1) with its human homologue BRAK and with the mouse  $\alpha$ -chemokines mCrg-2, mMig, mSDF-1, mBLC, mMIP2, mKC and mLIX. An additional five residues are present in KS1 and  
25 BRAK between cysteine 3 and cysteine 4 that have not previously been described for chemokines.

#### Detailed Description of the Invention

In one aspect, the present invention provides polynucleotides that were isolated  
30 from mammalian skin cells. As used herein, the term "polynucleotide" means a single or

double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and RNA molecules, both sense and anti-sense strands. The term comprehends cDNA, genomic DNA, recombinant DNA and wholly or partially synthesized nucleic acid molecules. A polynucleotide may consist of an entire gene, or a portion thereof. A  
5 gene is a DNA sequence that codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-  
10 Benion et al., "Anti-sense Techniques," *Methods in Enzymol.* 254(23):363-375, 1995; and Kawasaki et al., *Artific. Organs* 20(8):836-848, 1996.

Identification of genomic DNA and heterologous species DNAs can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an  
15 appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to the identified sequences and variants may be produced by conventional synthesis methods. All the polynucleotides provided by the present invention are isolated and  
20 purified, as those terms are commonly used in the art.

In specific embodiments, the polynucleotides of the present invention comprise a sequence selected from the group consisting of sequences provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511, and 514-623, and variants of the sequences of SEQ ID NOS: 1-119, 198-274, 349-372, 399-  
25 405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623. Polynucleotides that comprise complements of such sequences, reverse complements of such sequences, or reverse sequences of such sequences, together with variants of such sequences, are also provided.

The definition of the terms “complement,” “reverse complement,” and “reverse sequence,” as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

5	complement	3' TCCTGG 5'
	reverse complement	3' GGTCCT 5'
	reverse sequence	5' CCAGGA 3'.

As used herein, the term “complement” refers to sequences that are fully complementary to a sequence disclosed herein.

In another aspect, the present invention provides isolated polypeptides and functional portions of polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term “polypeptide” encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term “polypeptide encoded by a polynucleotide” as used herein, includes polypeptides encoded by a polynucleotide which comprises a partial isolated DNA sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, as well as variants of such sequences.

Polypeptides of the present invention may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512-513 and 624-725, and variants thereof. As  
5 used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

10 Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain  
15 biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such  
20 polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc.  
25 (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, T., *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequence



may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure. In certain preferred embodiments, described in detail below, the isolated polypeptides are incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. In certain preferred embodiments, variants of the inventive sequences retain certain, or all, of the functional characteristics of the inventive sequence. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% or 95% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The alignment and similarity of polypeptide sequences may be examined using the BLASTP and algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>)

under /blast/executables/ and are available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894 USA.

5 The FASTA and FASTX algorithms are available on the Internet at the ftp site ftp://ftp.Virginia.edu/pub/. The FASTA software package is also available from the University of Virginia by contacting David Hudson, Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The  
10 readme files for FASTA and FASTX v1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is also described in Pearson, and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.

15 The BLASTN algorithm version 2.0.4 [Feb-24-1998], 2.0.6 [Sept-16-1998] and 2.0.11 [Jan-20-2000], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm version 2.0.4, 2.0.6 and 2.0.11, set to the default parameters described in the documentation and distributed  
20 with the algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX is described in the publication of Altschul, *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments  
25 and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with default parameters thus: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero

invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional. The following running parameters are preferred for determination of  
 5 alignments and similarities using BLASTP that contribute to the E values and percentage identity for polypeptides: blastall -p blastp -d swissprot db -e 10 -G 1 -E 11 -r 1 -v 30 -b 30 -i queryseq -o results; and the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior)  
 10 [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions  
 15 of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using  
 20 appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a  
 25 queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is

thus 21/220 times 100, or 9.5%. The identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default

parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP  
5 algorithm set at the default parameters.

Variant polynucleotide sequences will generally hybridize to the recited polynucleotide sequences under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X  
10 SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide or polypeptide, respectively, comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO:  
15 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; or any of the polypeptides set out in SEQ ID NO: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725. The value of x may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising  
20 at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623, or their variants. Polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 120-197, 275-348,  
25 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a

250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623, or of a variant of one of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511  
5 and 514-623. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, or of a variant of one of the polypeptides provided  
10 in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725.

The inventive polynucleotides may be isolated by high throughput sequencing of cDNA libraries prepared from mammalian skin cells as described below in Example 1. Alternatively, oligonucleotide probes based on the sequences provided in SEQ ID NOS:  
15 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623 can be synthesized and used to identify positive clones in either cDNA or genomic DNA libraries from mammalian skin cells by means of hybridization or polymerase chain reaction (PCR) techniques. Probes can be shorter than the sequences provided herein but should be at least about 10, preferably at least about 15 and most  
20 preferably at least about 20 nucleotides in length. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR Technology*, Stockton Press: NY, 1989; (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor  
25 Laboratory Press, Cold Spring Harbor: New York, 1989). Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

In addition, DNA sequences of the present invention may be generated by synthetic means using techniques well known in the art. Equipment for automated synthesis of oligonucleotides is commercially available from suppliers such as Perkin

Elmer/Applied Biosystems Division (Foster City, California) and may be operated according to the manufacturer's instructions.

Since the polynucleotide sequences of the present invention have been derived from skin, they likely encode proteins that have important roles in growth and development of skin, and in responses of skin to tissue injury and inflammation as well as disease states. Some of the polynucleotides contain sequences that code for signal sequences, or transmembrane domains, which identify the protein products as secreted molecules or receptors. Such protein products are likely to be growth factors, cytokines, or their cognate receptors. Several of the polypeptide sequences have more than 25% similarity to known biologically important proteins and thus are likely to represent proteins having similar biological functions.

In particular, the inventive polypeptides have important roles in processes such as: induction of hair growth; differentiation of skin stem cells into specialized cell types; cell migration; cell proliferation and cell-cell interaction. The polypeptides are important in the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of the disclosed polypeptides act as modulators of immune responses, especially since immune cells are known to infiltrate skin during tissue insult causing growth and differentiation of skin cells. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of disease states not only within skin, but also in other tissues of the body. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

In one aspect, the present invention provides methods for using one or more of the inventive polypeptides or polynucleotides to treat disorders in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human.

In this aspect, the polypeptide or polynucleotide is generally present within a pharmaceutical or immunogenic composition. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above

sequences (or variants thereof), and a physiologically acceptable carrier. Immunogenic compositions may comprise one or more of the above polypeptides and a non-specific immune response amplifier, such as an adjuvant or a liposome, into which the polypeptide is incorporated.

- 5        Alternatively, a pharmaceutical or immunogenic composition of the present invention may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such compositions, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, and bacterial and viral expression systems.
- 10        Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system
- 5        (*e.g.*, vaccinia or other poxvirus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA into such expression systems are well known in the art. The DNA may also be "naked," as described, for example, in Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA
- 10        may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

- Routes and frequency of administration, as well as dosage, vary from individual to individual. In general, the pharmaceutical and immunogenic compositions may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous, or
- 5        subcutaneous), intranasally (*e.g.*, by aspiration) or orally. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg per kg of host, and preferably from about 100 pg to about 1 µg per kg of host. Suitable dose



sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax, or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of adjuvants may be employed in the immunogenic compositions of the invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *Mycobacterium tuberculosis*. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories, Detroit, Michigan), and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, New Jersey). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, and Quil A.

The polynucleotides of the present invention may also be used as markers for tissue, as chromosome markers or tags, in the identification of genetic disorders, and for the design of oligonucleotides for examination of expression patterns using techniques well known in the art, such as the microarray technology available from Affymetrix (Santa Clara, CA). Partial polynucleotide sequences disclosed herein may be employed to obtain full length genes by, for example, screening of DNA expression libraries using hybridization probes or PCR primers based on the inventive sequences.

The polypeptides provided by the present invention may additionally be used in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, in assays to quantitatively determine levels of protein or cognate corresponding ligand or receptor, as anti-inflammatory agents, and in compositions for skin, connective tissue and/or nerve tissue growth or regeneration. The present invention further provides methods for modulating expression of the inventive polypeptides, for example by inhibiting translation of the relevant polynucleotide. Translation of the relevant polynucleotide may be inhibited, for example, by introducing anti-sense expression vectors; by introducing antisense oligodeoxyribonucleotides or antisense phosphorothioate oligodeoxyribonucleotides; by introducing antisense oligoribonucleotides or antisense phosphorothioate oligoribonucleotides; or by other means which are well known in the art. Cell permeation and activity of antisense oligonucleotides can be enhanced by appropriate chemical modifications, such as the use of phenoxazine-substituted C-5 propynyl uracil oligonucleotides (Flanagan *et al.*, (1999) *Nat. Biotechnol.* 17 (1): 48-52) or 2'-O-(2-methoxy) ethyl (2'-MOE)-oligonucleotides (Zhang *et al.*, (2000) *Nat. Biotechnol.* 18: 862-867). The use of techniques involving antisense polynucleotides is well known in the art and is described, for example, in Robinson-Benion *et al.* (1995), Antisense techniques, *Methods in Enzymol.* 254 (23): 363-375 and Kawasaki *et al.* (1996), *Artific. Organs* 20 (8): 836-848.

The following Examples are offered by way of illustration and not by way of limitation.

#### Example 1

##### ISOLATION OF CDNA SEQUENCES FROM SKIN CELL EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed from specialized rodent or human skin cells as shown in Table 1.

Table 1

<u>Library</u>	<u>Skin cell type</u>	<u>Source</u>
DEPA	dermal papilla	rat

	SKTC	keratinocytes	human
	HNFF	neonatal foreskin fibroblast	human
	MEMS	embryonic skin	mouse
	KSCL	keratinocyte stem cell	mouse
5	TRAM	transit amplifying cells	mouse
	MFSE	epidermis	mouse
	HLEA	small epithelial airway cells	human
	HLEB	small epithelial airway cells	human
	HNKA	NK cells	human

10

These cDNA libraries were prepared as described below.

cDNA Library from Dermal Papilla (DEPA)

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and  
 15 the total RNA extracted from these cells using established protocols. Total RNA,  
 isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was  
 used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla,  
 California), according to the manufacturer's specifications. A cDNA expression library  
 was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda  
 20 ZAP cDNA library synthesis kit (Stratagene).

cDNA Library from Keratinocytes (SKTC)

Keratinocytes obtained from human neonatal foreskins (Mitra, R and Nikoleff, B  
 in *Handbook of Keratinocyte Methods*, pp. 17-24, 1994) were grown in serum-free  
 25 KSFM (BRL Life Technologies) and harvested along with differentiated cells ( $10^8$  cells).  
 Keratinocytes were allowed to differentiate by addition of fetal calf serum at a final  
 concentration of 10% to the culture medium and cells were harvested after 48 hours.  
 Total RNA was isolated from the two cell populations using TRIzol Reagent (BRL Life  
 Technologies) and used to obtain mRNA using a Poly(A) Quik mRNA isolation kit

(Stratagene). cDNAs expressed in differentiated keratinocytes were enriched by using a PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, California). Briefly, mRNA was obtained from either undifferentiated keratinocytes ("driver mRNA") or differentiated keratinocytes ("tester mRNA") and used to synthesize cDNA. The two  
5 populations of cDNA were separately digested with *RsaI* to obtain shorter, blunt-ended molecules. Two tester populations were created by ligating different adaptors at the cDNA ends and two successive rounds of hybridization were performed with an excess of driver cDNA. The adaptors allowed for PCR amplification of only the differentially expressed sequences which were then ligated into T-tailed pBluescript (Hadjeb, N and  
10 Berkowitz, GA, *BioTechniques* 20:20-22 1996), allowing for a blue/white selection of cells containing vector with inserts. White cells were isolated and used to obtain plasmid DNA for sequencing.

cDNA library from human neonatal fibroblasts (HNFF)

15 Human neonatal fibroblast cells were grown in culture from explants of human neonatal foreskin and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's  
20 specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA library from mouse embryonic skin (MEMS)

Embryonic skin was micro-dissected from day 13 post coitum Balb/c mice.  
25 Embryonic skin was washed in phosphate buffered saline and mRNA directly isolated from the tissue using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

30 cDNA library from mouse stem cells (KSCL) and transit amplifying (TRAM) cells

Pelts obtained from 1-2 day post-partum neonatal Balb/c mice were washed and incubated in trypsin (BRL Life Technologies) to separate the epidermis from the dermis. Epidermal tissue was disrupted to disperse cells, which were then resuspended in growth medium and centrifuged over Percoll density gradients prepared according to the manufacturer's protocol (Pharmacia, Sweden). Pelleted cells were labeled using Rhodamine 123 (Bertoncello I, Hodgson GS and Bradley TR, *Exp Hematol.* 13:999-1006, 1985), and analyzed by flow cytometry (Epics Elite Coulter Cytometry, Hialeah, Florida). Single cell suspensions of rhodamine-labeled murine keratinocytes were then labeled with a cross reactive anti-rat CD29 biotin monoclonal antibody (Pharminogen, San Diego, California; clone Ha2/5). Cells were washed and incubated with anti-mouse CD45 phycoerythrin conjugated monoclonal antibody (Pharminogen; clone 30F11.1, 10ug/ml) followed by labeling with streptavidin spectral red (Southern Biotechnology, Birmingham, Alabama). Sort gates were defined using listmode data to identify four populations: CD29 bright rhodamine dull CD45 negative cells; CD29 bright rhodamine bright CD45 negative cells; CD29 dull rhodamine bright CD45 negative cells; and CD29 dull rhodamine dull CD45 negative cells. Cells were sorted, pelleted and snap frozen prior to storage at -80°C. This protocol was followed multiple times to obtain sufficient cell numbers of each population to prepare cDNA libraries. Skin stem cells and transit amplifying cells are known to express CD29, the integrin  $\beta 1$  chain. CD45, a leukocyte specific antigen, was used as a marker for cells to be excluded in the isolation of skin stem cells and transit amplifying cells. Keratinocyte stem cells expel the rhodamine dye more efficiently than transit amplifying cells. The CD29 bright, rhodamine dull, CD45 negative population (putative keratinocyte stem cells; referred to as KSCL), and the CD29 bright, rhodamine bright, CD45 negative population (keratinocyte transit amplifying cells; referred to as TRAM) were sorted and mRNA was directly isolated from each cell population using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

*cDNA Library from Epithelial Cells (MFSE)*

Skin epidermis was removed from flaky skin *fsn* <sup>-/-</sup> mice (The Jackson Laboratory, Bar Harbour, ME), the cells dissociated and the resulting single cell suspension placed in culture. After four passages, the cells were harvested. Total RNA,  
5 isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD), was used to obtain mRNA using a Poly(A)Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. A cDNA expression library (referred to as the MFSE library) was then prepared from the mRNA by Reverse Transcriptase synthesis using a Lambda ZAP Express cDNA library synthesis kit (Stratagene, La Jolla,  
10 CA).

*cDNA Libraries from Human Small Airway Epithelial Cells (HLEA and HLEB)*

Human small airway epithelium cells SAEC (Cell line number CC-2547, Clonetics Normal Human Cell Systems, Cambrex Corporation, East Rutherford NJ)  
15 transformed with human papilloma virus E6E7 that was infected with the bacterium *Yersinia enterocolitica* (ATCC No. 51871, American Type Culture Collection, Manassas VA) and the long form of the Respiratory Syncytial Virus (RSV, ATCC No. VR26), were used as source of RNA to construct the libraries called HLEA and HLEB. Cells from the twelfth passage of SAEC cells were infected with *Y. enterocolitica* for 2 hours at an  
20 initial seed of 12.5 bacteria per cell. The cells were disinfected with gentamycin (100 µg/ml) for 2 hours and harvested 4 hours after infection. The cells were then infected with RSV at a moiety of infection of 0.7 for 1 hour and incubated for 6 and 24 hours. Cells were harvested and the RNA extracted following standard protocols.

Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA  
25 isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. Two cDNA expression libraries were then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

*cDNA Library from Epithelial Cells (HNKA)*

The subtracted cDNA library (HNKA) from human natural killer (NK) cells was constructed as follows. A NK library was first constructed using pooled RNA extracted from primary NK cells from multiple donors, stimulated for 4 or 20 hours with IL-2 (10 ng/ml), IL-12 (1 ng/ml), IL-15 (50 ng/ml), interferon alpha (IFN- $\alpha$ ; 1,000 U/ml) 5 immobilized anti-CD16 or immobilized anti-NAIL antibody, or from unstimulated cells. RNA was extracted following standard procedures. cDNA was prepared using a TimeSaver kit (Pharmacia, Uppsala, Sweden) following the manufacturer's protocol. The cDNA was ligated to *Bgl*III adaptors and size-selected using cDNA sizing columns 10 (Gibco BRL, Gaithersburg MD). The size-selected NK cDNA was ligated into a pDc 409 vector and transformed into *E. coli* DH105 cells. Single-stranded DNA was prepared from the plasmid library using a helper phage (Stratagene)

A second cDNA library (referred to as FF cDNA library) was constructed using fetal foreskin tissue. RNA was extracted and cDNA prepared following standard 15 protocols. The cDNA was ligated into the plasmid pBluescript following standard protocols. 10  $\mu$ g of the FF cDNA library was linearized with the restriction endonuclease *Not*I and used as template to synthesize biotin-labeled cRNA using SP6 polymerase.

The subtracted NK cell library (HNKA) was constructed as follows. The 20 biotinylated FF cRNA was mixed with the NK library, ethanol precipitated and resuspended in 5  $\mu$ l buffer (50 mM HEPES pH 7.4, 10 mM EDTA, 1.5 M NaCl, 0.2% SDS). After addition of 5  $\mu$ l formamide and heating to 95° for 1 min, the material was left to hybridize for 24 hours at 42°C. 90  $\mu$ l of 10 mM HEPES pH 7.3, 1 mM EDTA and 15  $\mu$ l streptavidin was added followed by an incubation for 20 min at 50°C. This 25 step was repeated again after extraction with phenol/chloroform.

To the final extracted aqueous phase, the following were added: NaCl to 0.2 M, 1  $\mu$ l glycogen and 2 volumes of ethanol. After an overnight precipitation at -20°C, the DNA was pelleted and resuspended in 10  $\mu$ l water. A second round of subtraction was performed as above and the DNA transformed into *E. coli* DH105.

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer.

5

### Example 2

#### CHARACTERIZATION OF ISOLATED cDNA SEQUENCES

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithms FASTA and/or BLASTN. The corresponding  
10 protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the computer algorithms FASTX and/or BLASTX. Comparisons of DNA sequences provided in SEQ ID NO: 1-119 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 120-197 to sequences in the SwissProt database (using FASTX)  
15 were made as of March 21, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 198-274 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 275-348 to sequences in the SwissProt database (using BLASTP) were made as of October 7, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 349-372 to sequences in the EMBL DNA database (using  
20 BLASTN) and amino acid sequences provided in SEQ ID NO: 373-398 to sequences in the SwissProt database (using BLASTP) were made as of January 23, 1999. Comparisons of polynucleotide sequences provided in SEQ ID NO: 418-455 and 466-487 to sequences in the EMBL DNA database (using BLASTN) and polypeptide sequences provided in SEQ ID NO: 456-463 and 488-509 to sequences in the SwissProt database  
25 (using BLASTP) were made as of April 23, 2000. Comparisons of polynucleotide sequences provided in SEQ ID NO: 510 and 511 to sequences in the EMBL DNA database (using BLASTN) and polypeptide sequences provided in SEQ ID NO: 512 and 513 to sequences in the SwissProt database (using BLASTP) were made as of July 11, 2000. Comparisons of polynucleotide sequences provided in SEQ ID NO: 514-623 to



sequences in the EMBL66 - HTGs + ENSEMBL (May 1, 2001) DNA database (using BLASTN) and polypeptide sequences provided in SEQ ID NO: 624-725 to sequences in the SP\_TR\_NRDB + ENSEMBL (April 30, 2001) database (using BLASTP) were made as of May 16, 2001.

5

Isolated cDNA sequences and their corresponding polypeptide sequences were computer analyzed for the presence of signal sequences identifying secreted molecules. Isolated cDNA sequences that have a signal sequence at a putative start site within the sequence are provided in SEQ ID NO: 1-44, 198-238, 349-358, 399, 418-434, 440-449 and 466-471, 516, 519, 520, 523-527, 531, 532, 535-537, 548, 555, 574-580, 585-587, 589, 593, 595, 596, 598-601, 605-607, 609, 612, 613, 615, 616 and 622. The cDNA sequences of SEQ ID NO: 1-6, 198-199, 349-352, 354, 356-358, 419-428, 430-433, 440-444, 446-448, 466, 468-470, 519, 520, 523, 524, 529, 531, 532, 535-537, 579, 585, 587, 598, 605, 609, 613 and 622 were determined to have less than 75% identity (determined as described above), to sequences in the EMBL database using the computer algorithms FASTA or BLASTN, as described above. The polypeptide sequences of SEQ ID NO: 120-125, 275-276, 373-380, 382, 456, 457, 460-462, 488-493, 633, 637, 642, 683, 685, 691, 693, 703, 706, 710, 714, 717, 718, 720, 721 and 725 were determined to have less than 75% identity (determined as described above) to sequences in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of the full-length cDNA sequences provided in SEQ ID NOS: 7-14, 200-231, 372, 418-422, 441-448, 514, 516, 557-561, 567, 568, 619 and 621. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 7-14, 200-231, 372, 514, 516, 557-561, 567, 568, 619 and 621 are provided in SEQ ID NOS: 126-133, 277-308, 396, 624, 626, 666-669, 674 and 724 respectively. The cDNA sequences of SEQ ID NO: 418-422 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 7 and 11-14, namely SEQ ID NO: 126 and 130-133, respectively. Comparison of the full-

length cDNA sequences with those in the EMBL database using the computer algorithm FASTA or BLASTN, as described above, revealed less than 75% identity (determined as described above) to known sequences, except for the polynucleotides in SEQ ID NOS: 516, 560 and 619. Comparison of the amino acid sequences provided in SEQ ID NOS: 126-133, 277-308, 666, 668, 669 and 724 with those in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above, revealed less than 75% identity (determined as described above) to known sequences.

Comparison of the polypeptide sequences corresponding to the cDNA sequences of SEQ ID NOS: 15-23 with those in the EMBL database using the computer algorithm FASTA database showed less than 75% identity (determined as described above) to known sequences. These polypeptide sequences are provided in SEQ ID NOS: 134-142.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of full-length cDNA sequences provided in SEQ ID NOS: 24-44, 232-238, 423-434, 449, 466, 468-470, 475, 476 and 484. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 24-44, 232-238, 429, 466, 468-470, 475, 476 and 484 are provided in SEQ ID NOS: 143-163, 309-315, 456, 488, 490-492, 497, 498 and 506, respectively. The cDNA sequences of SEQ ID NO: 423-428, 430-434 and 449 encode the same polypeptide sequences as the cDNA sequences of SEQ ID NO: 27-29, 34, 35, 37, 40-44 and 238, namely SEQ ID NO: 146-148, 153, 154, 156, 159-163 and 315, respectively. These polypeptide sequences were determined to have less than 75% identity, determined as described above to known sequences in the SwissProt database using the computer algorithm FASTX.

Isolated cDNA sequences having less than 75% identity to known expressed sequence tags (ESTs) or to other DNA sequences in the public database, or whose corresponding polypeptide sequence showed less than 75% identity to known protein sequences, were computer analyzed for the presence of transmembrane domains coding for putative membrane-bound molecules. Isolated cDNA sequences that have one or more transmembrane domain(s) within the sequence are provided in SEQ ID NOS: 45-63, 239-253, 359-364, 400-402, 435, 436, 450-452, 455, 470-472, 542, 553-555, 573,

576, 581, 592, 593, 595 and 606. The cDNA sequences of SEQ ID NOS: 45-48, 239-249, 359-361, 363, 450, 451, 455, 472, 473, 553-555, 573, 576 and 592 were found to have less than 75% identity (determined as described above) to sequences in the EMBL database, using the FASTA or BLASTN computer algorithms. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 45-48, 239-249, 359-361, 363, 450, 451, 472, 473, 553-555, 573 and 606 (provided in SEQ ID NOS: 164-167, 316-326, 383, 385-388, 407-408, 460, 461, 494, 495, 662, 663, 664, 679, 682 and 711 respectively) were found to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the FASTX or BLASTP database. The cDNA sequence of SEQ ID NO: 455 encodes the same polypeptide sequence as the cDNA sequence of SEQ ID NO: 359, namely SEQ ID NO: 383.

Comparison of the polypeptide sequences corresponding to the cDNA sequences of SEQ ID NOS: 49-63, 250-253, 436 and 452 with those in the SwissProt database showed less than 75% identity (determined as described above) to known sequences. These polypeptide sequences are provided in SEQ ID NOS: 168-182, 327-330, 457 and 462, respectively.

Using automated search programs to screen against sequences coding for molecules reported to be of therapeutic and/or diagnostic use, some of the cDNA sequences isolated as described above in Example 1 were determined to encode polypeptides that are family members of known protein families. A family member is here defined to have at least 25% identity in the translated polypeptide to a known protein or member of a protein family. These cDNA sequences are provided in SEQ ID NOS: 64-76, 254-264, 365-369, 403, 437-439, 453, 454, 475-487, 510, 511, 514-527, 529-531, 533-536, 538-546, 548, 549, 553-559, 562, 564, 565, 567, 569-575, 577-589, 591-602, 604-612, 616-618, 621 and 622. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 64-76, 254-264, 365-369, 403, 438, 439, 453, 475-487, 510 and 511, 514-527, 529-531, 533-536, 538-546, 548, 549, 553-559, 562, 564, 565, 567, 569-575, 577-589, 591-602, 604-612, 616-618, 621 and 622 are provided in SEQ ID NOS: 183-195, 331-341, 389-393, 409, 458, 459, 463, 497-509, 624-637, 639-641, 643-

646, 648-656, 658, 659, 662-668, 670, 672-681, 683-707, 709-717 and 721-725, respectively. The cDNA sequences of SEQ ID NO: 437 and 454 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 68 and 262, namely SEQ ID NO: 187 and 339, respectively. The cDNA sequences of SEQ ID NOS: 64-68, 254-264, 365-  
 5 369, 437-439, 453, 454, 475-478, 480-482, 484, 485, 487, 511, 514, 515, 517-520, 522, 523, 525, 529-531, 535, 536, 538, 541, 544-546, 549, 553-559, 564, 565, 567, 569-573, 579, 587, 588, 592, 597, 598, 602, 604, 605, 608-611, 617, 621 and 622 show less than 75% identity (determined as described above) to sequences in the EMBL database using the FASTA or BLASTN computer algorithms. Similarly, the amino acid sequences of  
 10 SEQ ID NOS: 183-195, 331-341, 389-393, 458, 459, 463, 497, 498, 503-505, 507-509, 512, 513, 628, 632, 633, 637, 640, 655, 662-666, 668, 672, 673, 676, 679, 683, 685, 688, 691, 693, 694, 702, 703, 706, 707, 710, 711, 713, 714, 717, 721, 722 and 725 show less than 75% identity to sequences in the SwissProt database.

15 The isolated cDNA sequences encode proteins that influence the growth, differentiation and activation of several cell types, and that may usefully be developed as agents for the treatment and diagnosis of skin wounds, cancers, growth and developmental defects, and inflammatory disease. The utility for certain of the proteins of the present invention, based on similarity to known proteins, is provided in Table 2  
 20 below, together with the location of signal peptides and transmembrane domains for certain of the inventive sequences:

Table 2  
 FUNCTIONS OF NOVEL PROTEINS

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
64, 372	183, 396	Slit, a secreted molecule required for central nervous system development
65	184	Immunoglobulin receptor family. About 40% of leucocyte membrane polypeptides contain immunoglobulin superfamily domains

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
66, 403 510	185, 409 512	RIP protein kinase, a serine/threonine kinase that contains a death domain to mediate apoptosis
67	186	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation
68, 437	187	Transforming growth factor alpha, a protein which binds epidermal growth factor receptor and stimulates growth and mobility of keratinocytes
69	188	DRS protein which has a secretion signal component and whose expression is suppressed in cells transformed by oncogenes
70	189	A33 receptor with immunoglobulin-like domains and is expressed in greater than 95% of colon tumors
71	190	Interleukin-12 alpha subunit, component of a cytokine that is important in the immune defense against intracellular pathogens. IL-12 also stimulates proliferation and differentiation of TH1 subset of lymphocytes
72	191	Tumor Necrosis Factor receptor family of proteins that are involved in the proliferation, differentiation and death of many cell types including B and T lymphocytes.
73	192	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
74	193	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors
75	194	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
76	195	Immunoglobulin receptor family
254	331	Receptor with immunoglobulin-like domains and homology to A33 receptor which is expressed in greater than 95% of colon tumors
255	332	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
256	333	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
257	334	Contains protein kinase and ankyrin domains. Possible role in cellular growth and differentiation.
258	335	Notch family proteins which are receptors involved in cellular differentiation.
259	336	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation.
260, 453	337, 463	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors.
261	338	Immunoglobulin receptor family
262	339	ADP/ATP transporter family member containing a calcium binding site.
263	340	Mouse CXC chemokine family members are regulators of epithelial, lymphoid, myeloid, stromal and neuronal cell migration and cancers, agents for the healing of cancers, neuro-degenerative diseases, wound healing, inflammatory autoimmune diseases like psoriasis, asthma, Crohns disease and as agents for the prevention of HIV-1 of leukocytes
264	341	Nucleotide-sugar transporter family member.
365	389	Transforming growth factor betas (TGF-betas) are secreted covalently linked to latent TGF-beta-binding proteins (LTBPs). LTBPs are deposited in the extracellular matrix and play a role in cell growth or differentiation.
366	390	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
367	391	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
368	392	Cell wall protein precursor. Are involved in cellular growth or differentiation.
369	393	HT protein is a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.
467	489	Myb proto-oncogene (c-Myb), involved in transcription regulation and activation of transcription

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
471	493	Chondroitin sulfotransferase, a member of the HNK-1 sulfotransferase family. These molecules are involved in the pathogenesis of arteriosclerosis, and proliferation of arterial smooth muscle cells during development of arteriosclerosis.
472	494	36 kDa nucleolar protein HNP36, a novel growth factor responsive gene expressed in the pituitary and parathyroid glands
475	497	Zinc protease is a matrix metalloproteinase whose activity is directed against components of the extracellular matrix and play an important role in the growth, metastasis and angiogenesis of tumors.
476	498	Diapophytoene dehydrogenase crtn-like molecule. This molecule is similar to the diapophytoene dehydrogenase crt molecule in a major photosynthesis gene cluster from the bacterium <i>Heliobacillus mobilis</i>
477	499	Protocadherin 3 family member, involved in cell to cell interactions.
478	500	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
479	501	Integrin family member. Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
480	502	Similar to secreted HT Protein, a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.
481	503	Agrin family member: Agrin is produced by motoneurons and induces the aggregation of nicotinic acetylcholine receptors.
482	504	Macrophage Scavenger Receptors bind to a variety of polyanionic ligands and display complex binding characteristics. They have been implicated in various macrophage-associated processes, including atherosclerosis.
483	505	Similar to GARP, a member of the family of leucine-rich repeat-containing proteins involved in platelet-endothelium interactions.
484	506	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		acid secretion.
485	507	Colony stimulating growth factor family.
486	508	Cytokine receptors
487	509	IL17 Receptor to Interleukin 17 (IL17), a T cell derived cytokine that may play a role in initiation or maintenance of the inflammatory response.
438	458	MEGF6, a protein containing multiple EGF-like-domains.
439	459	Protein kinase family member involved in signal transduction.
454		Peroxisomal calcium-dependent solute carrier, a new member of the mitochondrial transporter superfamily.
511	513	Serine/threonine kinase NEK1 is a NIMA-related protein kinase that phosphorylates serines and threonines, but also possesses tyrosine kinase activity. NEK1 has been implicated in the control of meiosis and belongs to the NIMA kinase subfamily.
514	624 626	Homologue isolated from rat dermal papilla of integrin alpha-11/beta-1 that is involved in muscle development and maintaining integrity of adult muscle and other adult tissues. Integrin alpha-11/beta-1 is a receptor for collagen and belongs to the integrin alpha chain family.
516	625	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 21; nucleotides 42 to 104).
517	626	Homologue isolated from a rat dermal papilla library of OASIS (old astrocyte specifically-induced substance) and that plays a role in regulation of the response of astrocytes to inflammation and trauma of the central nervous system (CNS) during gliosis. The OASIS gene encodes a putative transcription factor belonging to the cyclic AMP responsive element binding protein/activating transcription factor (CREB/ATF) gene family (Honma et al., Brain Res. Mol. Brain Res. 69:93-103, 1999).



P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
519	628	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 24; nucleotides 50 to 121).
520	630	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 35; nucleotides 67 to 171).
523	633	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 3 to 53).
524	634	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 20; nucleotides 13 to 72).
525, 534	635, 644	Homologue isolated from a rat dermal papilla library of leucyl-specific aminopeptidase, PILS-AP and that plays role in many physiological processes as a substrate-specific peptidase. PILS is a new member of the M1 family of Zn-dependent aminopeptidases that comprises members of closely related enzymes which are known to be involved in a variety of physiologically important processes.
526	636	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 26; nucleotides 114 to 191).
527	637	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 26; nucleotides 23 to 100).
529	639	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 37 to 87).
530	640	This is a homologue isolated from a rat dermal papilla library of a maturase that is involved in RNA splicing.
531	641	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 180 to 230).
532	642	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 32; nucleotides 245 to 340).
535	645	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 25; nucleotides 188 to 333).

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
536	646	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 21; nucleotides 185 to 247).
537	647	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 24; nucleotides 129 to 200).
541	651	This is a homologue isolated from a rat dermal papilla library of a hepatoma-derived growth factor (HDGF) that is involved in stimulation of cell proliferation.
542	652	This is a receptor-like molecule isolated from rat dermal papillae with two transmembrane domains (amino acid residues 20 to 40 and 58 to 78).
545	655	This is a homologue isolated from a rat dermal papilla library of Link protein (LP) and that is involved in bone formation. LP plays an essential role in endochondral bone formation by stabilizing the supramolecular assemblies of aggrecan and hyaluronan (Deak et al., Cytogenet. Cell Genet. 87:75-79, 1999).
548	658	This is a homologue isolated from a rat dermal papilla library of thrombospondin (TSP). It is a secreted protein with a signal peptide in amino acid residues 1 to 18 (nucleotides 210 to 263). TSP is an extracellular matrix glycoprotein whose expression has been associated with a variety of cellular processes including growth and embryogenesis (Laherty et al., J. Biol. Chem. 267:3,274-3,281, 1992).
553	662	This is a receptor-like molecule isolated from rat dermal papillae with a transmembrane domain (amino acid residues 434 to 454).
554	663	This is a receptor-like molecule isolated from rat dermal papillae with a transmembrane domain (amino acid residues 546 to 566).
555	664	This is a homologue isolated from a rat dermal papilla library of B7-like mouse GL50 (mGL50). It is a receptor-like molecule with a signal peptide in residues 1 to 24 (nucleotides 149 to 220) and a transmembrane domain in amino acid residues 262 to 282. GL50 is a specific ligand for the ICOS receptor and this interaction functions in lymphocyte costimulation (Ling et al., J. Immunol. 164:1,653-1,657, 2000).

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
557, 558, 561-572	666, 667, 670-678	These molecules are differentially expressed in stem cells but not in mature keratinocytes and are involved in developmental processes. They may be employed for diagnosis of tumors with an immature phenotype.
559	668	This is a homologue isolated from a mouse stem cell library of ABSENT IN MELANOMA 1 protein AIM1 and that can be used for diagnosis of tumours with an immature phenotype. AIM1 is a novel gene whose expression is associated with the experimental reversal of tumorigenicity of human malignant melanoma and belongs to the betagamma-crystallin superfamily (Ray et al., Proc. Natl. Acad. Sci. USA 94:3,229-3,234, 1997)
560	669	Homologue isolated from a mouse stem cell library of endothelin-converting enzyme 2 (ECE-2) and that can be used for diagnosis of tumours with an immature phenotype. Endothelins (ET) are a family of potent vasoactive peptides that are produced from biologically inactive intermediates, termed big endothelins, via a proteolytic processing at Trp21-Val/Ile22. ECE-2, that produces mature ET-1 from big ET-1 both in vitro and in transfected cells. ECE-2 acts as an intracellular enzyme responsible for the conversion of endogenously synthesized big ET-1 at the trans-Golgi network, where the vesicular fluid is acidified (Emoto and Yanagisawa, J. Biol. Chem. 270:15,262-15,268, 1995).
573	679	Mouse homologue of EGF-like molecule containing mucin-like hormone receptor 2 (EMR2). The isolated molecule contains three transmembrane regions: amino acid residues 20 to 40, 66 to 86 and 92 to 112. The epidermal growth factor (EGF)-TM7 proteins [EMR1 and EMR2, F4/80, and CD97] constitute a recently defined class B GPCR subfamily and are predominantly expressed on leukocytes. These molecules possess N-terminal EGF-like domains coupled to a seven-span transmembrane (7TM) moiety via a mucin-like spacer domain (Lin et al., Genomics 67:188-200, 2000).
574	680	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 238 to 288).
575	681	Mouse homologue of a glucocorticoid-inducible protein GIS5 with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 56-106)

P/N SEQ ID NO:	A/A SEQ ID NO:	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		residues 1 to 17; nucleotides 56-106).
576	682	This is a murine surface receptor-like molecule with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 1179 to 199) and a transmembrane domain (amino acid residues 179 to 199).
577	683	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 16; nucleotides 55 to 102).
578	684	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 22; nucleotides 12 to 77).
579	685	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 82 to 132).
580	686	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 20; nucleotides 20 to 79).
581	687	This is a murine receptor-like molecule with transmembrane domains at amino acid residues 50 to 70; 84 to 104; 116 to 136 and 179 to 198.
585	691	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 20; nucleotides 260 to 319).
586	695	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 22; nucleotides 295 to 360).
587	693	This is a mouse homologue of serotransferrin, also known as siderophilin or beta-1-metal binding globulin) and that is involved in iron transport. This homologue is a secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 19; nucleotides 43 to 99). Transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding of an anion, usually bicarbonate. It is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization. Serum transferrin may also have a further role in stimulating cell proliferation. Transferrin belongs to the transferrin family.

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
589	695	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 25; nucleotides 1 to 75).
592	697	This is a murine receptor-like molecule with a transmembrane domain in amino acid residues 52 to 72.
593	698	Mouse homologue of channel inducing factor (CHIF) that plays a role in ion transport. The mouse homologue has a signal peptide at the N-terminus of the predicted polypeptide (amino acid residues 1 to 20; nucleotides 102 to 161) and a transmembrane domain (amino acid residues 38 to 58). CHIF evokes a potassium channel activity (Attali et al., Proc. Natl. Acad. Sci. USA 92:6092-6096, 1995).
595	700	Homologue of hyaluronan receptor LYVE-1 that plays a role in hyaluronan uptake. This mouse homologue has the characteristic signal peptide and transmembrane domain of a receptor. A signal peptide was identified in the isolated molecule in amino acid residues 1 to 18 (nucleotides 62 to 115) and the transmembrane domain in amino acid residues 233 to 253. The extracellular matrix glycosaminoglycan hyaluronan (HA) is an abundant component of skin and mesenchymal tissues where it facilitates cell migration during wound healing, inflammation, and embryonic morphogenesis. Both during normal tissue homeostasis and particularly after tissue injury, HA is mobilized from these sites through lymphatic vessels to the lymph nodes where it is degraded before entering the circulation for rapid uptake by the liver. LYVE-1 is a receptor for HA on the lymph vessel wall and plays a role in the transport of HA from tissue to lymph (Banerji et al., J. Cell Biol. 144:789-801, 1999).
596	701	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 21; nucleotides 7 to 69).
598	703	Homologue of tumor-associated glycoprotein E4 (TAA1 or TAGE4) that belongs to the immunoglobulin superfamily. This molecule has a signal peptide at the N-terminus (amino acid residues 1 to 24; nucleotides 71 to 142) and is therefore a secreted protein.

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
599	704	Homologue of the LUNX protein, also known as nasopharyngeal carcinoma-related protein, tracheal epithelium enriched protein or plunc, that is expressed in epithelial cells in the airways. It has a signal peptide at the N-terminus (amino acid residues 1 to 19; nucleotides 39 to 95). Expression of LUNX is restricted to the trachea, upper airway, nasopharyngeal epithelium and salivary gland (Bingle and Bingle, Biochim. Biophys. Acta 1493:363-367, 2000).
600	705	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 23; nucleotides 136 to 204).
601	706	Homologue of prenylcysteine lyase (EC 4.4.1.18) and that is involved in degradation of prenylated proteins. It has a signal peptide at the N-terminus (amino acid residues 1 to 28; nucleotides 22 to 105). Prenylcysteine lyase is a specific enzyme involved in the final step of prenylcysteine metabolism in mammalian cells. The enzyme does not require NADPH as cofactor for prenylcysteine degradation, thus distinguishing it from cytochrome P450- and flavin-containing monooxygenases that catalyze S-oxidation of thioethers (Zhang et al., J. Biol. Chem. 274:35802-35808, 1999).
605	710	Homologue of endoplasmic reticulum protein 99 (ERp99), 94 kDa glucose-regulated protein (GRP94) and polymorphic tumor rejection antigen 1 (gp96). The isolated molecule has a signal peptide at the N-terminus (amino acid residue 1 to 21; nucleotides 1867 to 206). ERp99 is an abundant, conserved transmembrane glycoprotein of the endoplasmic reticulum membrane and homologous to the 90-kDa heat shock protein (hsp90) and the 94-kDa glucose regulated protein (GRP94) (Mazzarella and Green, J. Biol. Chem. 262:8875-8883, 1987).
606	711	Homologue of PILRalpha, formerly known as inhibitory receptor PIRIIalpha and that is involved in signal transduction in various cellular processes. This molecule contains a signal peptide at the N-terminal end (amino acid residues 1-21 and nucleotides 47 to 139) and a transmembrane domain at amino acid residues 191 to 211. SHP-1-mediated dephosphorylation of protein tyrosine

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		residues is central to the regulation of several cell signaling pathways. PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is paired with the truncated counterpart PILRbeta (Mousseau et al., J. Biol. Chem. 275:4467-4474, 2000).
607	712	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 18; nucleotides 38 to 91).
609	714	Homologue of retinal short-chain dehydrogenase/reductase retSDR2 that plays a role on retinal metabolism. It has a signal peptide at the N-terminus at amino acid residues 1 – 29 (nucleotides 302 to 388). Retinol dehydrogenases (RDH) catalyze the reduction of all-trans-retinal to all-trans-retinol within the photoreceptor outer segment in the regeneration of bleached visual pigments (Haeseleer et al., J. Biol. Chem. 273:21790-21799, 1998)
612	717	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 22; nucleotides 6 to 71).
613	718	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 25; nucleotides 210 to 284).
615	720	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 16; nucleotides 70 to 117).
616	721	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 18; nucleotides 1 to 54).

The locations of open reading frames (ORFs) within certain of the inventive cDNA sequences are shown in Table 3, below.

Table 3  
LOCATION OF OPEN READING FRAMES

SEQ ID NO Polynucleotide	ORF	SEQ ID NO Polypeptide
514	1-2,067	624
515	2-730	625
516	42-1,772	626
517	1-681	627
518	170-416	628
519	50-770	629
520	67-708	630
521	110-613	631
522	41-457	632
523	3-230	633
524	13-573	634
525	64-2,856	635
526	114-599	636
527	23-520	637
528	953-1,138	638
529	37-687	639
530	145-366	640
531	180-1,508	643
532	245-442	642
533	125-595	643
534	64-2,856	644
535	188-727	645
536	185-1,081	646
537	129-308	647
538	32-853	648
539	2-268	649
540	3-875	650
541	284-892	651
542	37-276	652
543	127-1,794	653
544	1-735	654
545	142-939	655
546	51-1,082	656
547	143-328	657
548	210-3,728	658
549	26-1,354	659
551	1,236-1,892	660
552	853-1,178	661



SEQ ID NO Polynucleotide	ORF	SEQ ID NO Polypeptide
553	54-1,356	662
554	637-2,244	663
555	149-1,072	664
556	18-449	665
557	275-1,171	666
558	453-1,133	667
559	104-2,449	668
560	463-687	669
562	1-1,107	670
563	2-883	671
564	188-2,902	672
565	3-524	673
567	2,584-3,996	674
569	1-960	675
570	315-599	676
571	1-414	677
572	806-1,912	678
573	120-752-	679
574	2381,359	680
575	56-1,456	681
576	13-645	682
577	55-1,323	683
578	12-698	684
579	82-810	685
580	20-586	686
581	65-808	687
582	369-761	688
583	1-769	689
584	164-1,321	690
585	260-1,489	691
586	295-1,131	692
587	43-2,136	693
588	1-1,203	694
589	1-525	695
591	1-584	696
592	1-522	697
593	102-368	698
594	1-517	699

SEQ ID NO Polynucleotide	ORF	SEQ ID NO Polypeptide
595	62-1,018	700
596	7-282	701
597	1-736	702
598	71-1,297	703
599	39-875	704
600	136-930	705
601	22-1,539	706
602	69-521	707
603	104-448	708
604	1-399	709
605	3,068-5,476	710
606	47-721	711
607	38-439	712
608	1-1,656	713
609	302-1,327	714
610	845-1,447	715
611	975-1,375	716
612	6-272	717
613	210-464	718
614	462-869	719
615	70-459	720
616	1-1,107	721
617	1-349	722
618	93-528	723
621	380-1,033	724
622	43-2,115	725

The cDNA sequences of SEQ ID NO: 514, 515, 516, 557, 558, 559, 560, 561,  
5 567, 568, 619 and 621 are extended sequences of SEQ ID NO: 479, 480, 353, 91, 108,  
82, 92, 81, 105, 90, 362 and 360, respectively. SEQ ID NO: 516, 520, 521, 523, 525,  
526, 529, 534-536, 541-543, 546, 548, 549, 557, 574, 575, 577-581, 584-587, 589, 593,  
595, 596, 598-601, 605, 607, 609, 610, 614, 616 and 622 represent full-length cDNA  
sequences.

The polynucleotide sequences of SEQ ID NOS: 77-117, 265-267, 404-405 and 557-611 are differentially expressed in either keratinocyte stem cells (KSCL) or in transit amplified cells (TRAM) on the basis of the number of times these sequences exclusively appear in either one of the above two libraries; more than 9 times in one and none in the other (Audic S. and Claverie J-M, *Genome Research*, 7:986-995, 1997). The sequences of SEQ ID NOS: 77-89, 265-267 and 365-369 were determined to have less than 75% identity to sequences in the EMBL database using the computer algorithm FASTA or BLASTN, as described above. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 77-117, 265-267, 404-405 and 557-611 are provided in SEQ ID NOS: 666-718. The amino acid sequences of SEQ ID NOS: 666, 668, 669, 671-673, 675, 676, 679, 682, 683, 685, 688, 690, 691, 693, 694, 702, 703, 706-708, 710, 711, 713 and 714 show less than 75% identity to sequences in the SwissProt database.

The polypeptides encoded by these polynucleotide sequences have utility as markers for identification and isolation of these cell types, and antibodies against these proteins may be usefully employed in the isolation and enrichment of these cells from complex mixtures of cells. Isolated polynucleotides and their corresponding proteins exclusive to the stem cell population can be used as drug targets to cause alterations in regulation of growth and differentiation of skin cells, or in gene targeting to transport specific therapeutic molecules to skin stem cells.

20

### Example 3

#### ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF muTR1

The human homolog of muTR1 (SEQ ID NO: 68), obtained as described above in Example 1, was isolated by screening 50,000 pfu's of an oligo dT primed HeLa cell cDNA library. Plaque lifts, hybridization, and screening were performed using standard molecular biology techniques (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). The determined cDNA sequence of the isolated human homolog (huTR1) is provided in SEQ ID NO: 118, with the corresponding

25

polypeptide sequence being provided in SEQ ID NO: 196. The library was screened using an [ $\alpha$   $^{32}$ P]-dCTP labeled double stranded cDNA probe corresponding to nucleotides 1 to 459 of the coding region within SEQ ID NO: 118.

5       \*\*The polypeptide sequence of huTR1 has regions similar to Transforming Growth Factor-alpha, indicating that this protein functions like an epidermal growth factor (EGF). EGF family members exist in a functional form as small peptides. Alignment of the functional peptides of the EGF family with SEQ ID NO: 196 revealed that an internal segment of SEQ ID NO: 196 (amino acids 54-104) shows greater than 40% identity to the active peptides of EGF, TGF-alpha and Epiregulin. The active  
10       peptides of the EGF family are sufficient for activity and contain several conserved residues critical for the maintenance of this activity. These residues are retained in huTR1. This EGF-like protein will serve to stimulate keratinocyte growth and motility, and to inhibit the growth of epithelial-derived cancer cells. This novel gene and its encoded protein may thus be used as agents for the healing of wounds and regulators of  
15       epithelial-derived cancers.

#### Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for huTR1 was performed by probing human tissue mRNA blots (Clontech) with a probe comprising  
20       nucleotides 93-673 of SEQ ID NO: 118, radioactively labeled with [ $\alpha$   $^{32}$ P]-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huTR1 was 3.5-4kb in size and was observed to be most abundant in heart and placenta, with expression at lower levels being observed in spleen, thymus, prostate and ovary (Fig. 1).

25       The high abundance of mRNA for huTR1 in the heart and placenta indicates a role for huTR1 in the formation or maintenance of blood vessels, as heart and placental tissues have an increased abundance of blood vessels, and therefore endothelial cells, compared to other tissues in the body. This, in turn, demonstrates a role for huTR1 in angiogenesis and vascularization of tumors. This is supported by the ability of

Transforming Growth Factor-alpha and EGF to induce *de novo* development of blood vessels (Schreiber, *et al.*, *Science* 232:1250-1253, 1986) and stimulate DNA synthesis in endothelial cells (Schreiber, *et al.*, *Science* 232:1250-1253, 1986), and their over-expression in a variety of human tumors.

5

Purification of muTR1 and huTR1

Polynucleotides 177-329 of muTR1 (SEQ ID NO: 268), encoding amino acids 53-103 of muTR1 (SEQ ID NO: 342), and polynucleotides 208-360 of huTR1 (SEQ ID NO: 269), encoding amino acids 54-104 of huTR1 (SEQ ID NO: 343), were cloned into  
0 the bacterial expression vector pProEX HT (BRL Life Technologies), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook *et al.*, *Ibid*.

Starter cultures of these recombinant XL1-Blue *E. coli* were grown overnight at 37°C in Terrific broth containing 100 µg/ml ampicillin. This culture was spun down and  
5 used to inoculate 500 ml culture of Terrific broth containing 100 µg/ml ampicillin. Cultures were grown until the OD<sub>595</sub> of the cells was between 0.4 and 0.8, whereupon IPTG was added to 1 mM. Cells were induced overnight and bacteria were harvested by centrifugation.

Both the polypeptide of muTR1 (SEQ ID NO: 342; referred to as muTR1a) and  
20 that of huTR1 (SEQ ID NO: 343; referred to as huTR1a) were expressed in insoluble inclusion bodies. In order to purify the polypeptides muTR1a and huTR1a, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM beta mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at  
25 95W for 4 x 15 seconds and then centrifuged for 15 minutes at 14,000 rpm to pellet the inclusion bodies.

The resulting pellet was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated on ice for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14,000 rpm for 15 minutes at 4 °C and the supernatant discarded. The pellet was once

more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M Guanidine HCl, 0.5 M NaCl, 20 mM Tris HCl, pH 8.0), sonicated at 95 W for 4 x 15 seconds and then centrifuged for 20 minutes at 14,000 rpm and 4 °C to remove debris. The supernatant was stored at 4 °C until use.

Polypeptides muTR1a and huTR1a were purified by virtue of the N-terminal 6x Histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating Sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's recommended protocol. In order to refold the proteins once purified, the protein solution was added to 5x its volume of refolding buffer (1 mM EDTA, 1.25 mM reduced glutathione, 0.25 mM oxidised glutathione, 20 mM Tris-HCl, pH 8.0) over a period of 1 hour at 4 °C. The refolding buffer was stirred rapidly during this time, and stirring continued at 4 °C overnight. The refolded proteins were then concentrated by ultrafiltration using standard protocols.

#### Biological Activities of Polypeptides muTR1a and huTR1a

muTR1 and huTR1 are novel members of the EGF family, which includes EGF, TGF $\alpha$ , epiregulin and others. These growth factors are known to act as ligands for the EGF receptor. The pathway of EGF receptor activation is well documented. Upon binding of a ligand to the EGF receptor, a cascade of events follows, including the phosphorylation of proteins known as MAP kinases. The phosphorylation of MAP kinase can thus be used as a marker of EGF receptor activation. Monoclonal antibodies exist which recognize the phosphorylated forms of 2 MAP kinase proteins – ERK1 and ERK2.

In order to examine whether purified polypeptides of muTR1a and huTR1a act as a ligand for the EGF receptor, cells from the human epidermal carcinoma cell line A431 (American Type Culture Collection, No. CRL-1555, Manassas, Virginia) were seeded into 6 well plates, serum starved for 24 hours, and then stimulated with purified muTR1a or huTR1a for 5 minutes in serum free conditions. As a positive control, cells were

stimulated in the same way with 10 to 100 ng/ml TGF-alpha or EGF. As a negative control, cells were stimulated with PBS containing varying amounts of LPS. Cells were immediately lysed and protein concentration of the lysates estimated by Bradford assay. 15 µg of protein from each sample was loaded onto 12% SDS-PAGE gels. The proteins  
5 were then transferred to PVDF membrane using standard techniques.

For Western blotting, membranes were incubated in blocking buffer (10mM Tris-HCl, pH 7.6, 100 mM NaCl, 0.1% Tween-20, 5% non-fat milk) for 1 hour at room temperature. Rabbit anti-Active MAP kinase pAb (Promega, Madison, Wisconsin) was added to 50 ng/ml in blocking buffer and incubated overnight at 4 °C. Membranes were  
10 washed for 30 mins in blocking buffer minus non-fat milk before being incubated with anti rabbit IgG-HRP antibody, at a 1:3500 dilution in blocking buffer, for 1 hour at room temperature. Membranes were washed for 30 minutes in blocking buffer minus non-fat milk, then once for 5 minutes in blocking buffer minus non-fat milk and 0.1% Tween-20. Membranes were then exposed to ECL reagents for 2 min, and then autoradiographed for  
15 5 to 30 min.

As shown in Fig. 2, both muTR1a and huTR1a were found to induce the phosphorylation of ERK1 and ERK2 over background levels, indicating that muTR1 and huTR1 act as ligands for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor. As shown in Fig. 11, huTR1a was also  
20 demonstrated to induce the phosphorylation of ERK1 and ERK2 in CV1/EBNA kidney epithelial cells in culture, as compared with the negative control. These assays were conducted as described above. This indicates that huTR1a acts as a ligand for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor in HeLa and CV1/EBNA cells.

25 The ability of muTR1a to stimulate the growth of neonatal foreskin (NF) keratinocytes was determined as follows. NF keratinocytes derived from surgical discards were cultured in KSFM (BRL Life Technologies) supplemented with bovine pituitary extract (BPE) and epidermal growth factor (EGF). The assay was performed in 96 well flat-bottomed plates in 0.1 ml unsupplemented KSFM. MuTR1a, human

transforming growth factor alpha (huTGF $\alpha$ ) or PBS-BSA was titrated into the plates and  $1 \times 10^3$  NF keratinocytes were added to each well. The plates were incubated for 5 days in an atmosphere of 5% CO<sub>2</sub> at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in  
5 Fig. 3, both muTR1a and the positive control human TGF $\alpha$  stimulated the growth of NF keratinocytes, whereas the negative control, PBS-BSA, did not.

The ability of muTR1a and huTR1a to stimulate the growth of a transformed human keratinocyte cell line, HaCaT, was determined as follows. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (BRL Life Technologies)  
0 supplemented with 0.2% FCS. MuTR1a, huTR1a and PBS-BSA were titrated into the plates and  $1 \times 10^3$  HaCaT cells were added to each well. The plates were incubated for 5 days in an atmosphere containing 10% CO<sub>2</sub> at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 4, both muTR1a and huTR1a stimulated the growth of HaCaT  
5 cells, whereas the negative control PBS-BSA did not.

The ability of muTR1a and huTR1a to inhibit the growth of A431 cells was determined as follows. Polypeptides muTR1a (SEQ ID NO: 342) and huTR1a (SEQ ID NO: 343) and PBS-BSA were titrated as described previously (*J. Cell. Biol.* 93:1-4, 1982), and cell death was determined using the MTT dye reduction as described  
0 previously (*J. Imm. Meth.* 93:157-165, 1986). Both muTR1a and huTR1a were found to inhibit the growth of A431 cells, whereas the negative control PBS-BSA did not (Fig. 5).

These results indicate that muTR1 and huTR1 stimulate keratinocyte growth and motility, inhibit the growth of epithelial-derived cancer cells, and play a role in angiogenesis and vascularization of tumors. This novel gene and its encoded protein may  
5 thus be developed as agents for the healing of wounds, angiogenesis and regulators of epithelial-derived cancers.



#### Upregulation of huTR1 and mRNA expression

HeLa cells (human cervical adenocarcinoma) were seeded in 10 cm dishes at a concentration of  $1 \times 10^6$  cells per dish. After incubation overnight, media was removed and replaced with media containing 100 ng/ml of muTR1, huTR1, huTGF $\alpha$ , or PBS as a negative control. After 18 hours, media was removed and the cells lysed in 2 ml of TRIzol reagent (Gibco BRL Life Technologies, Gaithersburg, Maryland). Total RNA was isolated according to the manufacturer's instructions. To identify mRNA levels of huTR1 from the cDNA samples, 1  $\mu$ l of cDNA was used in a standard PCR reaction. After cycling for 30 cycles, 5  $\mu$ l of each PCR reaction was removed and separated on a 1.5% agarose gel. Bands were visualized by ethidium bromide staining. As can be seen from Fig. 12, both mouse and human TR1 up-regulate the mRNA levels of huTR1 as compared with cells stimulated with the negative control of PBS. Furthermore, TGF $\alpha$  can also up-regulate the mRNA levels of huTR1.

These results indicate that TR1 is able to sustain its own mRNA expression and subsequent protein expression, and thus is expected to be able to contribute to the progression of diseases such as psoriasis where high levels of cytokine expression are involved in the pathology of the disease. Furthermore, since TGF $\alpha$  can up-regulate the expression of huTR1, the up-regulation of TR1 mRNA may be critical to the mode of action of TGF $\alpha$ .

#### Serum response element reporter gene assay

The serum response element (SRE) is a promoter element required for the regulation of many cellular immediate-early genes by growth. Studies have demonstrated that the activity of the SRE can be regulated by the MAP kinase signaling pathway. Two cell lines, PC12 (rat pheochromocytoma – neural tumor) and HaCaT (human transformed keratinocytes), containing eight SRE upstream of an SV40 promoter and luciferase reporter gene were developed in-house.  $5 \times 10^3$  cells were aliquoted per well of 96 well plate and grown for 24 hours in their respective media. HaCaT SRE cells were grown in 5% fetal bovine serum (FBS) in D-MEM supplemented with 2mM L-glutamine (Sigma,

St. Louis, Missouri), 1mM sodium pyruvate (BRL Life Technologies), 0.77mM L-asparagine (Sigma), 0.2mM arginine (Sigma), 160mM penicillin G (Sigma), 70mM dihydrostreptomycin (Roche Molecular Biochemicals, Basel, Switzerland), and 0.5 mg/ml geneticin (BRL Life Technologies). PC12 SRE cells were grown in 5% fetal bovine serum in Ham F12 media supplemented with 0.4 mg/ml geneticin (BRL Life Technologies). Media was then changed to 0.1% FBS and incubated for a further 24 hours. Cells were then stimulated with a titration of TR1 from 1 µg/ml. A single dose of basic fibroblast growth factor at 100 ng/ml (R&D Systems, Minneapolis, Minnesota) or epidermal growth factor at 10 ng/ml (BRL Life Technologies) was used as a positive control. Cells were incubated in the presence of muTR1 or positive control for 6 hours, washed twice in PBS and lysed with 40 µl of lysis buffer (Promega). 10 µl was transferred to a 96 well plate and 10 µl of luciferase substrate (Promega) added by direct injection into each well by a Victor<sup>2</sup> fluorimeter (Wallac), the plate was shaken and the luminescence for each well read at 3x1 sec Intervals. Fold induction of SRE was calculated using the following equation: Fold induction of SRE = Mean relative luminescence of agonist/Mean relative luminescence of negative control.

As shown in Fig. 13, muTR1 activated the SRE in both PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells. This indicates that HaCaT and PC-12 cells are able to respond to muTR1 protein and elicit a response. In the case of HaCaT cells, this is a growth response. In the case of PC-12 cells, this may be a growth, a growth inhibition, differentiation, or migration response. Thus, TR1 may be important in the development of neural cells or their differentiation into specific neural subsets. TR1 may also be important in the development and progression of neural tumors.

#### Inhibition by the EGF receptor assay

The HaCaT growth assay was conducted as previously described, with the following modifications. Concurrently with the addition of EGF and TR1 to the media, anti-EGF Receptor (EGFR) antibody (Promega, Madison, Wisconsin) or the negative

control antibody, mouse IgG (PharMingen, San Diego, California), were added at a concentration of 62.5 ng/ml.

As seen in Fig. 14, an antibody which blocks the function of the EGFR inhibited the mitogenicity of TR1 on HaCaT cells. This indicates that the EGFR is crucial for transmission of the TR1 mitogenic signal on HaCaT cells. TR1 may bind directly to the EGF receptor. TR1 may also bind to any other members of the EGFR family (for example, ErbB-2, -3, and/or -4) that are capable of heterodimerizing with the EGFR.

#### Splice variants of huTR1

A variant of huTR1 was isolated from the same library as huTR1, following the same protocols. The sequence referred to as huTR1-1 (also known as TR1 $\delta$ ) is a splice variant of huTR1 and consists of the ORF of huTR1 minus amino acids 15 to 44 and 87 to 137. These deletions have the effect of deleting part of the signal sequence and following amino terminal linker sequence, residues following the second cysteine residue of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, huTR1-1 is an intracellular form of huTR1. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF $\alpha$ . The determined nucleotide sequence of huTR1-1, is given in SEQ ID NO: 412, with the corresponding amino acid sequence being provided in SEQ ID NO: 415.

Four additional splice variants of huTr1 were isolated by PCR on first strand cDNA made from RNA isolated from HeLa cells by standard protocols. These splice variants of huTR1 are referred to as TR1-2 (also known as TR1 $\beta$ ), TR1-3 (also known as TR1 $\gamma$ ), TR1 $\epsilon$  and TR1 $\phi$ .

TR1-2 consists of the ORF of huTR1 minus amino acids 95 to 137. This deletion has the effect of deleting the transmembrane domain. Therefore TR1-2 is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other

EGF family members, including EGF and TGF $\alpha$ . The determined cDNA sequence of TR1-2 is given in SEQ ID NO: 410 and the corresponding amino acid sequence in SEQ ID NO: 413.

5 TR1-3 consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 86 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence, residues following the second cysteine of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1-3 is also a secreted form of huTR1 and functions as an agonist or an  
10 antagonist to huTR1 or other EGF family members, including EGF and TGF $\alpha$ . The determined cDNA sequence of TR1-3 is given in SEQ ID NO: 411 and the corresponding amino acid sequence is SEQ ID NO: 414.

TR1 $\epsilon$  consists of the ORF of huTR1 minus amino acids 86 to 136. This deletion has the effect of deleting residues following the second cysteine of the EGF motif and the  
15 transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1 $\epsilon$  is also a secreted form of huTR1 and functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF $\alpha$ . The determined cDNA sequence of TR1 $\epsilon$  is given in SEQ ID NO: 371 and the corresponding  
20 polypeptide sequence in SEQ ID NO: 395.

TR1 $\phi$  consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 95 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence and the transmembrane domain. Therefore TR1 $\phi$  is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF $\alpha$ . The determined nucleotide sequence of TR1 $\phi$  is given in SEQ ID NO: 416 and the corresponding polypeptide sequence in SEQ ID NO: 417.

10

#### Example 4

##### IDENTIFICATION, ISOLATION AND CHARACTERIZATION OF DP3

A partial cDNA fragment, referred to as DP3, was identified by differential display RT-PCR (modified from Liang P and Pardee AB, *Science* 257:967-971, 1992) using mRNA from cultured rat dermal papilla and footpad fibroblast cells, isolated by standard cell biology techniques. This double stranded cDNA was labeled with [ $\alpha^{32}$ P]-dCTP and used to identify a full length DP3 clone by screening 400,000 pfu's of an oligo dT-primed rat dermal papilla cDNA library. The determined full-length cDNA sequence for DP3 is provided in SEQ ID NO: 119, with the corresponding amino acid sequence being provided in SEQ ID NO: 197. Plaque lifts, hybridization and screening were performed using standard molecular biology techniques.

20

#### Example 5

##### ISOLATION AND CHARACTERIZATION OF KS1

##### 25 Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for muKS1 (SEQ ID NO: 263) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [ $\alpha^{32}$ P]-dCTP. Prehybridization, hybridization, washing, and probe labeling were performed as

described in Sambrook, *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was observed to be most abundant in brain, lung, or any muscle, and heart. Expression could also be detected in lower intestine, skin, bone marrow, and kidney. No detectable signal was found in testis, spleen, liver, thymus, stomach.

5

#### Human homologue of muKS1

MuKS1 (SEQ ID NO: 263) was used to search the EMBL database (Release 50, plus updates to June, 1998) to identify human EST homologues. The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and  
10 AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified in AA643952 and HS1301003 when translated. Combination of all three ESTs identified huKS1 (SEQ ID NO: 270) and translated polypeptide SEQ ID NO: 344. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

15

#### Identification of KSCL009274 cDNA sequence

A directionally cloned cDNA library was constructed from immature murine keratinocytes and submitted for high-throughput sequencing. Sequence data from a clone designated KDCL009274 showed 35% identity over 72 amino acids with rat macrophage  
20 inflammatory protein-2B (MIP-2B) and 32% identity over 72 amino acids with its murine homologue. The insert of 1633bp (SEQ ID NO: 464; Fig. 15A) contained an open reading frame of 300bp with a 5' untranslated region of 202bp and a 3' untranslated region of 1161bp. A poly-adenylation signal of AATAAA is present 19 base-pairs upstream of the poly-A tail. The mature polypeptide (SEQ ID NO: 465) is 77 amino  
25 acids in length containing 4 conserved cysteines with no ELR motif. The putative signal peptide cleavage site between GLY 22 and Ser 23 was predicted by the hydrophobicity profile. This putative chemokine was identical to KS1. The full length sequence was screened against the EMBL database using the BLAST program and showed some identity at the nucleotide level with human EST clones AA643952, AA865643, and

HS1301003, respectively. A recently described human CXC chemokine, BRAK, has some identity with KS1 at the protein level. The alignment of KS1 (referred to in Fig. 15B as KLF-1), BRAK, and other murine  $\alpha$ -chemokines is shown in Fig. 15B. The phylogenetic relationship between KS1 and other  $\alpha$ -chemokine family members was determined using the Phylip program. KS1 and BRAK demonstrate a high degree of divergence from the other  $\alpha$ -chemokines, supporting the relatively low homology shown in the multiple alignment.

Bacterial expression and purification of muKS1 and huKS1

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 271), encoding amino acids 23-99 of polypeptide muKS1 (SEQ ID NO: 345), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 272), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 346), were cloned into the bacterial expression vector pET-16b (Novagen, Madison, Wisconsin), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid.*

Starter cultures of recombinant BL 21 (DE3) *E. coli* (Novagen) containing SEQ ID NO: 271 (muKS1a) and SEQ ID NO: 272 (huKS1a) were grown in NZY broth containing 100  $\mu$ g/ml ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100  $\mu$ g/ml ampicillin. Cultures were grown until the OD<sub>595</sub> of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an induced band of approximately 15kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM  $\beta$ -Mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14000 rpm for 15 minutes at 4°C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged, and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95W for 4 x 15 seconds and centrifuged for 10 minutes at 18000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM tris-HCl pH 7.5 + 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 + 10% (w/v) glycerol. Preparations obtained were greater than 95% pure as determined by SDS-PAGE. Endotoxin contamination of purified proteins were determined using a limulus amebocyte lysate assay kit (BIO Whittaker, Walkersville, MD). Endotoxin levels were <0.1 ng/μg of protein. Internal amino acid sequencing was performed on tryptic peptides of KS1.

An Fc fusion protein was produced by expression in HEK 293 T cells. 35μg of KLF-1pIGFc DNA to transfect  $6 \times 10^6$  cells per flask, 200 mls of Fc containing supernatant was produced. The Fc fusion protein was isolated by chromatography using an Affiprep protein A resin (0.3 ml column, Biorad). After loading, the column was washed with 15 mls of PBS, followed by a 5 ml wash of 50 mM Na citrate pH 5.0. The protein was then eluted with 6 column volumes of 50 mM Na citrate pH 2.5, collecting 0.3 ml fractions in tubes containing 60μl of 2M Tris-HCl pH 8.0. Fractions were analyzed by SDS-PAGE.

Peptide sequencing of muKS1 and huKS1



Bacterially expressed muKS1 and huKS1 were separated on polyacrylamide gels and induced bands of 15 kDa were identified. The predicted size of muKS1 is 9.4 kDa. To obtain the amino acid sequence of the 15 kDa bands, 20 µg recombinant muKS1 and huKS1 was resolved by SDS-PAGE and electroblotted onto Immobilon PVDF membrane (Millipore, Bedford, Massachusetts). Internal amino acid sequencing was performed on tryptic peptides of muKS1 and huKS1 by the Protein Sequencing Unit at the University of Auckland, New Zealand.

The determined amino acid sequences for muKS1 and huKS1 are given in SEQ ID NOS: 397 and 398, respectively. These amino acid sequences confirmed that the determined sequences are identical to those established on the basis of the cDNA sequences. The size discrepancy has previously been reported for other chemokines (Richmond A, Balentien E, Thomas HG, Flaggs G, Barton DE, Spiess J, Bordon R, Francke U, Derynck R, "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-thromboglobulin," *EMBO J.* 7:2025-2033, 1988; Liao F, Rabin RL, Yannelli JR, Koniaris LG, Vanguri P, Farber JM, "Human Nig chemokine: biochemical and functional characterization," *J. Exp. Med.* 182:1301-1314, 1995). The isoelectric focusing point of these proteins was predicted to be 10.26 using DNASIS (HITACHI Software Engineering, San Francisco, California). Recombinant Fc tagged KS1 expressed and purified using protein A affinity column chromatography revealed a homogenous protein with a molecular mass of 42kDa.

#### Oxidative burst assay

Oxidative burst assays were used to determine responding cell types.  $1 \times 10^7$  PBMC cells were resuspended in 5 ml HBSS, 20mM HEPES, 0.5% BSA and incubated for 30 minutes at 37°C with 5 µl 5 mM dichloro-dihydrofluorescein diacetate (H<sub>2</sub>DCFDA, Molecular Probes, Eugene, Oregon).  $2 \times 10^5$  H<sub>2</sub>DCFDA-labeled cells were loaded in each well of a flat-bottomed 96 well plate. 10 µl of each agonist was added simultaneously into the well of the flat-bottomed plate to give final concentrations of 100 ng/ml (fMLP was used at 10 µM). The plate was then read on a Victor<sup>2</sup> 1420

multilabel counter (Wallac, Turku, Finland) with a 485 nm excitation wavelength and 535 nm emission wavelength. Relative fluorescence was measured at 5 minute intervals over 60 minutes.

A pronounced respiratory burst was identified in PBMC with a 2.5 fold difference  
5 between control treated cells (TR1) and cells treated with 100 ng/ml muKS1 (Fig. 8). Human stromal derived factor-1 $\alpha$  (SDF1 $\alpha$ ) (100 ng/ml) and 10  $\mu$ M formyl-Met-Leu-Phe (fMLP) were used as positive controls.

#### Chemotaxis assay

0 Cell migration in response to muKS1 was tested using a 48 well Boyden's chamber (Neuro Probe Inc., Cabin John, Maryland) as described in the manufacturer's protocol. In brief, agonists were diluted in HBSS, 20mM HEPES, 0.5% BSA and added to the bottom wells of the chemotactic chamber. THP-1 cells were re-suspended in the same buffer at  $3 \times 10^5$  cells per 50  $\mu$ l. Top and bottom wells were separated by a PVP-  
5 free polycarbonate filter with a 5  $\mu$ m pore size for monocytes or 3  $\mu$ m pore size for lymphocytes. Cells were added to the top well and the chamber incubated for 2 hours for monocytes and 4 hours for lymphocytes in a 5% CO<sub>2</sub> humidified incubator at 37°C. After incubation, the filter was fixed and cells scraped from the upper surface. The filter was then stained with Diff-Quick (Dade International Inc., Miami, Florida) and the  
10 number of migrating cells counted in five randomly selected high power fields. The results are expressed as a migration index (the number of test migrated cells divided by the number of control migrated cells).

Using this assay, muKS1 was tested against T cells and THP-1 cells. MuKS1 induced a titrateable chemotactic effect on THP-1 cells from 0.01 ng/ml to 100 ng/ml  
15 (Fig. 9). Human SDF1 $\alpha$  was used as a positive control and gave an equivalent migration. MuKS1 was also tested against IL-2 activated T cells. However, no migration was evidence for muKS1 even at high concentrations, whereas SDF-1 $\alpha$  provided an obvious titrateable chemotactic stimulus. Therefore, muKS1 appears to be chemotactic for THP-1 cells but not for IL-2 activated T cells at the concentrations tested.

Flow cytometric binding studies

Binding of KLF-1 to THP-1 and Jurkat cells was tested in the following manner. THP-1 or Jurkat cells ( $5 \times 10^6$ ) were resuspended in 3 mls of wash buffer (2% FBS and 0.2% sodium azide in PBS) and pelleted at 4°C, 200 x g for 5 minutes. Cells were then blocked with 0.5% mouse and goat sera for 30 minutes on ice. Cells were washed, pelleted, resuspended in 50 µl of KLF-1Fc at 10 µg/ml and incubated for 30 minutes on ice. After incubation, the cells were prepared as before and resuspended in 50 µl of goat anti-human IgG biotin (Southern Biotechnology Associates, AL) at 10 µg/ml and incubated for 30 minutes on ice. Finally, cells were washed, pelleted and resuspended in 50 µl of streptavidin-RPE (Southern Biotechnology Associates, AL) at 10 µg/ml and incubated for a further 30 minutes on ice in the dark. Cells were washed and resuspended in 250 µl of wash buffer and stained with 1 µl of 10 µg/ml propidium iodide (Sigma) to exclude any dead cells. Purified Fc fragment (10 µg/ml) was used as a negative control in place of KLF-1Fc to determine non-specific binding. Ten thousand gated events were analyzed on log scale using PE filter arrangement with peak transmittance at 575 nm and bandwidth of 10 nm on an Elite cell sorter (Coulter Cytometry).

The respiratory burst and migration assays indicated that KS1 is active on monocytes and not T cells; therefore, the KS1 Fc fusion protein was tested in a binding study with THP-1 and Jurkat T cells. KS1 Fc showed a marked positive shift on THP-1 cells compared with the Fc fragment alone. In contrast, KS1 demonstrated no positive binding with Jurkat cells in an identical experiment.

Full length sequence of muKS1 clone

The nucleotide sequence of muKS1 was extended by determining the base sequence of additional ESTs. Combination of all the ESTs identified the full-length muKS1 (SEQ ID NO: 370) and the corresponding translated polypeptide sequence in SEQ ID NO: 394.

Analysis of human RNA transcripts by Northern blotting

Northern blot analysis to determine the size and distribution of mRNA for the human homologue of muKS1 was performed by probing human tissue blots (Clontech, Palo Alto, California) with a radioactively labeled probe consisting of nucleotides 1 to 288 of huKS1 (SEQ ID NO: 270). Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huKS1 was 1.6 kb in size and was observed to be most abundance in kidney, liver, colon, small intestine, and spleen. Expression could also be detected in pancreas, skeletal muscle, placenta, brain, heart, prostate, and thymus. No detectable signal was found in lung, ovary, and testis.

Analysis of human RNA transcripts in tumor tissue by Northern blotting

Northern blot analysis to determine distribution of huKS1 in cancer tissue was performed as described previously by probing tumor panel blots (Invitrogen, Carlsbad, California). These blots make a direct comparison between normal and tumor tissue. MRNA was observed in normal uterine and cervical tissue but not in the respective tumor tissue. In contrast, expression was up-regulated in breast tumor and down-regulated in normal breast tissue. No detectable signal was found in either ovary or ovarian tumors.

Injection of bacterially recombinant muKS1 into C3H/HeJ mice

Eighteen C3H/HeJ mice were divided into 3 groups and injected intraperitoneally with muKS1, GV14B, or phosphate buffered saline (PBS). GV14B is a bacterially expressed recombinant protein used as a negative control. Group 1 mice were injected with 50 µg of muKS1 in 1 ml of PBS; Group 2 mice were injected with 50 µg of GV14B in 1 ml of PBS; and Group 3 mice with 1 ml of PBS. After 18 hours, the cells in the peritoneal cavity of the mice were isolated by intraperitoneal lavage with 2 x 4 ml washes with harvest solution (0.02% EDTA in PBS). Viable cells were counted from individual

mice from each group. Mice injected with 50 µg of muKS1 had on average a 3-fold increase in cell numbers (Fig. 10).

20 µg of bacterial recombinant muKS1 was injected subcutaneously into the left hind foot of three C3H/HeJ mice. The same volume of PBS was injected into the same site on the right-hand side of the same animal. After 18 hours, mice were examined for inflammation. All mice showed a red swelling in the foot pad injected with bacterially recombinant KS1. From histology, sites injected with muKS1 had an inflammatory response of a mixed phenotype with mononuclear and polymorphonuclear cells present.

#### 10 Injection of bacterially expressed muKS1a into nude mice

To determine whether T cells are required for the inflammatory response, the experiment was repeated using nude mice. Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20ug of bacterially expressed muKS1a (SEQ ID NO: 345) was injected subcutaneously in the left hind foot, ear and left-hand side of the back. The same volume of phosphate buffered saline was injected in the same sites but on the right-hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline. Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

25

#### Discussion

Chemokines are a large superfamily of highly basic secreted proteins with a broad number of functions (Baggiolini, *et al.*, *Annu. Rev. Immunol.*, 15:675-705, 1997; Ward, *et al.*, *Immunity*, 9:1-11, 1998; Horuk, *Nature*, 393:524-525, 1998). The polypeptide

sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore be expected to stimulate leukocyte, epithelial, stromal, and neuronal cell migration; promote angiogenesis and vascular development; promote neuronal patterning, hemopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes; and promotion of migration in wound healing events. It has recently been shown that receptors to chemokines act as co-receptors for HIV-1 infection of CD4+ cells (Cairns, *et al.*, *Nature Medicine*, 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury, *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid, stromal, and neuronal cells migration and cancers; as agents for the treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases such as psoriasis, asthma and Crohn's disease for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

We have also shown that muKS1 promotes a quantifiable increase in cell numbers in the peritoneal cavity of C3H/HeJ mice injected with muKS1. Furthermore, we have shown that muKS1 induces an oxidative burst in human peripheral blood mononuclear cells and migration in the human monocyte leukemia cell line, THP-1, suggesting that monocyte/macrophages are one of the responsive cell types for KS1. In addition to this, we demonstrated that huKS1 was expressed at high levels in a number of non-lymphoid tissues, such as the colon and small intestine, and in breast tumors. It was also expressed in normal uterine and cervical tissue, but was completely down-regulated in their respective tumors. It has recently been shown that non-ELR chemokines have demonstrated angiostatic properties. IP-10 and Mig, two non-ELR chemokines, have previously been shown to be up-regulated during regression of tumors (Tannenbaum CS, Tubbs R, Armstrong D, Finke JH, Bukowski RM, Hamilton TA, "The CXC Chemokines IP-10 and Mig are necessary for IL-12-mediated regression of the mouse RENCA

tumor," *J. Immunol.* 161: 927-932, 1998), with levels of expression inversely correlating with tumor size (Kanegane C, Sgadari C, Kanegane H, Teruya-Feldstine J, Yao O, Gupta G, Farber JM, Liao F, Liu L, Tosato G, "Contribution of the CXC Chemokines IP-10 and Mig to the antitumor effects of IL-12," *J. Leuko. Biol.* 64: 384-392, 1998).  
5 Furthermore, neutralizing antibodies to IP-10 and Mig would reduce the anti-tumor effect, indicating the contribution these molecules make to the anti-tumor effects. Therefore, it is expected that in the case of cervical and uterine tumors, KS1 would have similar properties.

The data demonstrates that KS1 is involved in cell migration showing that one of  
10 the responsive cell types is monocyte/macrophage. The human expression data in conjunction with the *in vitro* and *in vivo* biology demonstrates that this molecule may be a useful regulator in cell migration, and as an agent for the treatment of inflammatory diseases, such as Crohn's disease, ulcerative colitis, and rheumatoid arthritis; and cancers, such as cervical adenocarcinoma, uterine leiomyoma, and breast invasive ductal  
15 carcinoma.

#### Example 6

##### CHARACTERIZATION OF KS2

KS2 contains a transmembrane domain and may function as either a membrane-  
20 bound ligand or a receptor. Northern analysis indicated that the mRNA for KS2 was expressed in the mouse keratinocyte cell line, Pam212, consistent with the cDNA being identified in mouse keratinocytes.

##### Mammalian Expression

25 To express KS2, the extracellular domain was fused to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This was performed by cloning polynucleotides 20-664 of KS2 (SEQ ID NO: 273), encoding amino acids 1-215 of polypeptide KS2 (SEQ ID NO: 347), into the mammalian expression vector pcDNA3 (Invitrogen, NV Leek, Netherlands), to the amino terminus of

the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This construct was transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid.* The Fc fusion construct of KS2a was expressed by transfecting Cos-1 cells in 5 x T175 flasks with 180 µg of KS1a using DEAE-dextran. The supernatant was harvested after seven days and passed over a Ni-NTA column. Bound KS2a was eluted from the column and dialysed against PBS.

The ability of the Fc fusion polypeptide of KS2a to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes was determined as follows. A single cell suspension was prepared from the spleens of BALB/c mice and washed into DMEM (GIBCO-BRL) supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 0.77 mM L-asparagine, 0.2 mM L-arginine, 160 mM penicillin G, 70 mM dihydrostreptomycin sulfate,  $5 \times 10^{-2}$  mM beta mercaptoethanol and 5% FCS (cDMEM). Splenocytes ( $4 \times 10^6$ /ml) were stimulated with 2 µg/ml concanavalin A for 24 hrs at 37°C in 10% CO<sub>2</sub>. The cells were harvested from the culture, washed 3 times in cDMEM and resuspended in cDMEM supplemented with 10 ng/ml rhuIL-2 at  $1 \times 10^5$  cells/ml. The assay was performed in 96 well round bottomed plates in 0.2 ml cDMEM. The Fc fusion polypeptide of KS2a, PBS, LPS and BSA were titrated into the plates and  $1 \times 10^4$  activated T cells (0.1 ml) were added to each well. The plates were incubated for 2 days in an atmosphere containing 10% CO<sub>2</sub> at 37°C. The degree of proliferation was determined by pulsing the cells with 0.25 uCi/ml tritiated thymidine for the final 4 hrs of culture after which the cells were harvested onto glass fiber filtermats and the degree of thymidine incorporation determined by standard liquid scintillation techniques. As shown in Fig. 6, the Fc fusion polypeptide of KS2a was found to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes, whereas the negative controls PBS, BSA and LPS did not.

This data demonstrates that KS2 is expressed in skin keratinocytes and inhibits the growth of cytokine induced splenocytes. This indicates a role for KS2 in the regulation of skin inflammation and malignancy.



## Example 7

Characterization of KS3

KS3 encodes a polypeptide of 40 amino acids (SEQ ID NO: 129). KS3 contains a signal sequence of 23 amino acids that would result in a mature polypeptide of 17 amino acids (SEQ ID NO: 348; referred to as KS3a).

KS3a was prepared synthetically (Chiron Technologies, Victoria, Australia) and observed to enhance transferrin-induced growth of the rat intestinal epithelial cells IEC-18 cells. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (GIBCO-BRL Life Technologies) supplemented with 0.2% FCS. KS3a (SEQ ID NO: 348), apo-Transferrin, media and PBS-BSA were titrated either alone, with 750 ng/ml Apo-transferrin or with 750 ng/ml BSA, into the plates and  $1 \times 10^3$  IEC-18 cells were added to each well. The plates were incubated for 5 days at 37°C in an atmosphere containing 10% CO<sub>2</sub>. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 7, KS3a plus Apo-transferrin was found to enhance transferrin-induced growth of IEC-18 cells, whereas KS3a alone or PBS-BSA did not, indicating that KS3a and Apo-transferrin act synergistically to induce the growth of IEC-18 cells.

This data indicates that KS3 is epithelial derived and stimulates the growth of epithelial cells of the intestine. This suggests a role for KS3 in wound healing, protection from radiation- or drug-induced intestinal disease, and integrity of the epithelium of the intestine.

SEQ ID NOS: 1-725 are set out in the attached Sequence Listing. The codes for polynucleotide and polypeptide sequences used in the attached Sequence Listing confirm to WIPO Standard ST.25 (1988), Appendix 2.

All references cited herein, including patent references and non-patent references, are hereby incorporated by reference in their entireties.

Although the present invention has been described in terms of specific embodiments, changes and modifications can be carried out without departing from the

scope of the invention which is intended to be limited only by the scope of the appended claims.

We claim:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (b) complements of the sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (c) reverse complements of the sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (d) reverse sequences of the sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (e) sequences having at least a 99% probability of being the same as a sequence selected from any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters described above; (f) nucleotide sequences having at least 75% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (g) nucleotide sequences having at least 90% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (h) nucleotide sequences having at least 95% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (g) open reading frames of SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623.
2. An expression vector comprising an isolated polynucleotide of claim 1.
3. A host cell transformed with an expression vector of claim 2.
4. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 488-509, 512, 513 and 624-725; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters described above; (c) sequences having

at least 75% identity to a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 90% identity to a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (e) sequences having at least 95% identity to a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (f) sequences encoded by a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725.

5. An isolated polynucleotide encoding a polypeptide of claim 4.

6. An expression vector comprising an isolated polynucleotide of claim 5.

7. A host cell transformed with an expression vector of claim 6.

8. An isolated polypeptide comprising at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 196, 488-509, 512, 513 and 624-725; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters described above; (c) sequences having at least 75% identity to a sequence provided in SEQ ID NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above; (d) sequences having at least 90% identity to a sequence provided in SEQ ID NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above; (e) sequences having at least 95% identity to a sequence provided in SEQ ID

NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above; and (f) sequences encoded by a sequence provided in SEQ ID NOS: 466-487, 510, 511 and 514-623.

9. A method for stimulating keratinocyte growth and motility in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

10. The method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; (b) sequences having at least about 50% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least about 75% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least about 90% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

11. A method for inhibiting the growth of cancer cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

12. The method of claim 11, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90%

identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

13. A method for modulating angiogenesis in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

14. The method of claim 13, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196..

15. A method for inhibiting angiogenesis and vascularization of tumors in a patient, comprising administering to a patient a composition comprising a polypeptide of claim 4.

16. The method of claim 15, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS:

187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

17. A method for modulating skin inflammation in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

18. The method of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 338 and 347; and (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

19. A method for stimulating the growth of epithelial cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

20. The method of claim 19, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 129 and 348; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity

test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

21. A method for inhibiting the binding of HIV-1 to leukocytes in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

22. The method of claim 21, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

23. A method for treating an inflammatory disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

24. The method of claim 23, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90%



identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

25. A method for treating cancer in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

26. The method of claim 25, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

27. A method for treating a neurological disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

28. The method of claim 27, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397

and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

## SEQUENCE LISTING

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Watson, James D.  
 Strachan, Lorna  
 Sleeman, Matthew  
 Onrust, Rene  
 Murison, James G.  
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<213> mouse

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<210> 23  
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<212> DNA  
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<400> 23

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<212> DNA  
<213> Rat

<400> 24

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<212> DNA  
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<400> 25

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&lt;210&gt; 26

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 26

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&lt;210&gt; 27

&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 27

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&lt;210&gt; 28

&lt;211&gt; 1123

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 28

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 <212> DNA  
 <213> Rat

<220>

<400> 30

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 <212> DNA  
 <213> Human

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<210> 32  
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 <212> DNA  
 <213> mouse

<400> 32  
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 <212> DNA  
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<212> DNA  
 <213> mouse  
 <220>  
 <221> unsure  
 <222> (644) ... (644)

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 <212> DNA  
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 aagaagtacc agctgaacct gccatcttac cctgacacag agtgtgtcta ccgtctacag 720  
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 aaaaaaaaaa aaactcg 797

<210> 36  
 <211> 896  
 <212> DNA  
 <213> mouse

<400> 36  
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 cccatcccag atttgcttag tttgtctccc aatgtgctgg actttaaga cagggaaatgg 180  
 agaagcagat ggatgcttca gtttcagtca tttttggctc tatagtgate tctgccttcc 240  
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 tgggttaggag cctggctagg tatctttgag agatggatgc agctggctac tcaggcaggt 480  
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 gaagtgggta aggccagctg aaggccagtc agggcaactt agatgtagcc tggcttctac 600  
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 <212> DNA  
 <213> mouse

<400> 37  
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 gttcttcaga cactctctggc ctttgcagtt accgtttatg gcatagttca tatcgaggg 240  
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 aatcacccat ctttttatgt gtttaacccat cgtggtcgag tgctgttccg gccttcagat 360  
 gcaacaaatt cttcaaacct agatgcattg tcctctaata catcgttgaa gttacgaaag 420  
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<210> 38  
 <211> 766  
 <212> DNA  
 <213> mouse

<400> 38  
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 cgggcggcat ccccgggccg ccgcacgcac aggcgggcgc cctccttgcc tccctgctcc 180  
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 ataagacaaa ttatatattg ctatgaagct cttcttacca gggtcagttt ttacatttta 660  
 tagctgtgtg tgaaggcctt ccagatgtga gatccagctc gcctgcgcac cagacttcat 720  
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<210> 39  
 <211> 480  
 <212> DNA



&lt;213&gt; mouse

&lt;400&gt; 39

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cagatatgca cagaccttt gaattgtgac tactaattat agcaggggac ttgggtaccc 480

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&lt;210&gt; 40

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 40

```

ggcacgagat tagcggctcc tcagccagc aaatcctcca ctcatcatgc ttctctctgc 60
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aatgatgcc acagaaatcc tttattcaca tgtgggttaa cctgtcccgg cacaccccag 180
cagcaacagc accctgaatc aagccaggaa tggaggcagg catttcagta gcactggact 240
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aa 962

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&lt;210&gt; 41

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 41

```

ggcacgaggg tagtcgaatg tccgggctgc ggacgctgct ggggctgggg ctgctgggtg 60
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tggacattcc ttcccttggt gaaatgcccc cagaggatgg gatgtagaga agggaaaccc 540
tagcggaatc caaccagact tactcatctc actgacggca cccaagaagt ctgcaactca 600
ctttactggc cgatatcatt accttggggg togetttgta ccactgctc tagagaagaa 660
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aaaaaaaaact cgag 794

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<210> 42  
 <211> 1152  
 <212> DNA  
 <213> mouse

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 tctgtgacta tagggaggtt agcacttttt ctaattggaa ttcttctctg tctgtggcc 180  
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 aatttttttg agtccgtgcc tgtgggtggc agtcctgagc ctacagctga agcagtgtct 780  
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 ccagggaact ccaggtggga actgctgtgg cagtgaagtc agcccggaca gacactgcca 960  
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 gcctgccag cc 1152

<210> 43  
 <211> 446  
 <212> DNA  
 <213> mouse

<400> 43  
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 actcctggag ctggagttag agacaatggg gagctgcctt gtggatgttg ggaattgaac 180  
 ccaggctctc tggagaaata accagtgcctc ttaaccacta agccatctca acagcccca 240  
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 ctaatataga ttatttatga attcaggtgg cttaatggta tatgcatgaa ttagtagtaa 360  
 aacaagaact agggccagca agtggcttaa ggggtgcctgc taaccatctc agccacctga 420  
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<210> 44  
 <211> 391  
 <212> DNA  
 <213> mouse

<400> 44  
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 acacagagac agatgccgtg agctccagaa gtaattggacg gccccccact gctggcgctg 180  
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<210> 45

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 45

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ctctttcccc	gaaaagaagt	atgtggacca	gagagaccgg	gctggggggc	cccatgcctt	420
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&lt;210&gt; 46

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 46

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agggggatca	gaaatggggg	ctcccatctc	tggtgtctgc	ccagtccctc	caggtgggct	180
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ccccag						306

&lt;210&gt; 47

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 47

gaaaaactcg	aggacgtca	ctggacagct	tgggcttttt	tcagttgatt	ttatggtttg	60
catctttctc	tttctctttt	tctgtttctt	gttccccctt	ccccttttcc	tggtgagaaa	120
gcacatatta	ctgagccatt	gcaagcaatg	ggaggggtcc	acaatgacac	acacacacac	180
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ttgcaagtga	tcttccatgc	agtatgaaac	atgcagacag	cactggagtg	tggaagagtg	360
gagcttgccc	cacaagtctc	tcggggatgt	tgtactcttg	tgtgtgttta	cagtatcatg	420
gctgttacat	ctactggtc					439

&lt;210&gt; 48

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (3)...(3)

&lt;400&gt; 48

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 <212> DNA  
 <213> Rat

<400> 49  
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<210> 50  
 <211> 337  
 <212> DNA  
 <213> Rat

<220>

<400> 50  
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 ctccagaacat atacaacctg tacgagcaag tcagctacaa ctgtttcatc gcccggggcc 240  
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<210> 51  
 <211> 371  
 <212> DNA  
 <213> Rat

<220>  
 <221> unsure  
 <222> (80) ... (80)

<221> unsure  
 <222> (312) ... (312)

<221> unsure  
 <222> (319) ... (319)

<221> unsure  
 <222> (353) ... (354)

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 <211> 228  
 <212> DNA  
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<400> 52  
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 gagatgcac actgacaaca gagatggacc agtacagaat tacctgct 228

<210> 53  
 <211> 361  
 <212> DNA  
 <213> Human

<400> 53  
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 cattgtgctt aataatacca agactaagca ccataaccac gaaatactaa tgtaaagatt 300  
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<210> 54  
 <211> 403  
 <212> DNA  
 <213> Human

<220>

<400> 54  
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 aagtcctgta cacgggaaga cactgggaca tacacttgta tgg 403

<210> 55  
 <211> 413  
 <212> DNA  
 <213> Human

<400> 55  
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 tgggcatgaa gtgcacgcgc tgtgggggag acgacaaagt gaagaaggcc cgtatagcca 180  
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<210> 56

<211> 452  
 <212> DNA  
 <213> Human

<400> 56  
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<210> 57  
 <211> 190  
 <212> DNA  
 <213> Rat

<220>

<400> 57  
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 cagtgtgcaa catatataaa acagaaatac taactctaca ggcagtatgt cgacgcgggc 180  
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<210> 58  
 <211> 413  
 <212> DNA  
 <213> mouse

<400> 58  
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 <213> mouse

<220>  
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 <222> (213) ... (213)

<221> unsure  
 <222> (223) ... (223)

<221> unsure  
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&lt;222&gt; (243) ... (243)

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&lt;210&gt; 60

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 60

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&lt;210&gt; 61

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; unsure

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&lt;400&gt; 61

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taa						363

&lt;210&gt; 62

&lt;211&gt; 399

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 62

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&lt;210&gt; 63

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 <213> mouse

<220>

<400> 63

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<400> 64

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&lt;210&gt; 65

&lt;211&gt; 3008

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(435)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 65

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&lt;210&gt; 66

&lt;211&gt; 1888

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1690)...(1690)

&lt;221&gt; unsure

&lt;222&gt; (1755)...(1755)

&lt;221&gt; unsure

&lt;222&gt; (1864)...(1864)

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 <212> DNA  
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 <211> 355  
 <212> DNA  
 <213> Rat

<400> 69						
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 <211> 1421  
 <212> DNA  
 <213> Human

<400> 70						
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<211> 378  
 <212> DNA  
 <213> Human

<400> 71  
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 acccgcaaga caaaacaact ggttcttgcc agcctctaga gaaatcccag aacactcagc 240  
 cctgacacgt taataccctg cacagatcag aggtctgctgg ccacacagac tcaccaagcc 300  
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 tacctgcccc ggcgggcg 378

<210> 72  
 <211> 267  
 <212> DNA  
 <213> mouse

<400> 72  
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<210> 73  
 <211> 1633  
 <212> DNA  
 <213> Mouse

<220>  
 <221> misc\_feature  
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 <223> n = A,T,C or G

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<210> 74  
 <211> 1252  
 <212> DNA  
 <213> mouse

<400> 74						
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<210> 75  
 <211> 2411  
 <212> DNA  
 <213> mouse

<400> 75						
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<210> 76  
 <211> 1335  
 <212> DNA  
 <213> mouse

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<210> 77  
 <211> 440  
 <212> DNA  
 <213> mouse

<220>  
 <221> misc\_feature  
 <222> (1)...(440)  
 <223> n = A,T,C or G

<400> 77  
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<210> 78  
 <211> 204  
 <212> DNA  
 <213> mouse

<400> 78  
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 <212> DNA  
 <213> mouse

<220>  
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<400> 79  
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<210> 80  
 <211> 214  
 <212> DNA  
 <213> mouse

<400> 80  
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<210> 81  
 <211> 152  
 <212> DNA  
 <213> mouse

<220>

<400> 81  
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 ctgatggagc tgaacggtat ccctaaaag ta 152

<210> 82  
 <211> 181  
 <212> DNA  
 <213> mouse

<220>

<400> 82  
 ttcctagtgt gatgagaagc tccggaggag gcaggagaaa gcagggccccc gccctccct 60  
 gggctctccac ccaccacacg ccgctaaggc cacctgttct cccatggaga tgatgaagaa 120  
 gctcatagct ggacaaggcc cggaaacctca gccagtaac cgacctactt ccgcctggg 180  
 a 181

<210> 83  
 <211> 332  
 <212> DNA  
 <213> mouse

<220>

<400> 83  
 tatagagatg gtgatgtaat gggccagggt gtaagcttca acctggggga ttttgctggt 60  
 tttgttgttt ccctgtgtag ccctaacaag cctgtgtaga ccaggctggc ttttaactttg 120  
 cagatgacat tcacgtctac ttctctctgt gttgggggta tgggtctgca cacctgcca 180  
 ggcctaggct gggggatttt gaagtatctt agattatgga gtagaccag agtttgcaag 240  
 tatctgcttt aaagtgcac ataaacatag cctcctgacc atcttccaca gtgggaccct 300  
 gatctggcct ctccctggaa gaagagagaa ag 332

<210> 84  
 <211> 213  
 <212> DNA  
 <213> mouse

<400> 84  
 gcaggcagat aacaatgatt actggacaga gtgcttcaac gcattggaac aggggaggca 60  
 atatgtggat aatccacag gcgggaaagt ggacgaggct ctggtgagaa gtgccaccgt 120  
 acattgttgg ccgcacagca acgtgctgga cacaagcatg ctctcatccc cagatgtggt 180  
 gcgcagtctg ctgtccctgc agcccttctt gca 213

<210> 85  
 <211> 273

```

<212> DNA
<213> mouse

<220>
<221> misc_feature
<222> (1)...(273)
<223> n = A,T,C or G

<400> 85
cgggctctct ctctcctcct tccccgcctc ttctgcctcc cctgcctgga actctgatga      60
ggaggggacca ggtggtcagg caccacagtc tgatcaggac tcctgtggcc tccagagttt      120
cantcccccg tccatcctga agcgggctcc tcgggagcgt ccaggtcang tggcctttaa      180
cggcatcanc gtctactatt tcccacggtg ccaaggattc accagtgtgc ccaagccgtg      240
gtggctgtac cctgggnatg gcttctcggc aca                                     273

<210> 86
<211> 218
<212> DNA
<213> mouse

<400> 86
ctcagccgcc tgctctgggg gctggagggt ctcccaactta actgtgtctg ccgttcaggg      60
ggctcaccca gtgtgcgct acacagaggt ttccctcca gctccagtc gtctgccta      120
ctccttctat aaccgcctcc aagagctggc ctcaactgtt ccccgccggg ataagccctg      180
cccagcctat gtggagccta tgactgtggg ttgtcacc                               218

<210> 87
<211> 335
<212> DNA
<213> mouse

<400> 87
gagggtgggg gggtgcatag cctgcctgca attgctgccg ctgggcttaa cgtgttgtga      60
gctggccggg ttcttacaca gcagcacctg ccatggagcc tggccacaag gccactcaga      120
gctgggtgga cagagtgtga ccagaaactc cctgtgggtt ctgataaagg attctcccat      180
aggcaagggt cagagaacct gggcctcctg ttctcaggga ggcctgtcta tccccagcct      240
ctgagctggt tcgtcctagt tggtagttaa agtggcatag cctccttgag gcctctgatg      300
tgggaagggg acagaattgc aattattctt gcatg                                     335

<210> 88
<211> 410
<212> DNA
<213> mouse

<400> 88
aaaccccgcc aggaacaaaa taccggtgta tcggcctttac tgaatgcatt tattcccaaa      60
gggaaactga aaagcaacct agggacactg taagcagaaa gctgaggctt ttaaaaaccc      120
accttggaac tgtaacttgg gaggttccca cacaccaggg gctgtgcac gtgaaattct      180
gtctcctgag acgctgagaa acccttcctt gcagctataa tgggcctggc cggccagtgt      240
ggagctgtag ctccacga cgtagccctc aggaacttca ggagggatgc cacagtctat      300
ttctgaaaac aaaaccgtgt caacttcttt actttacaaa tgcaagtttt cagaatccac      360
catctctctg caccatacc ccatgcctca caccacagac cctgtgttag                               410

<210> 89
<211> 279
<212> DNA
<213> mouse

```

&lt;220&gt;

&lt;400&gt; 89

gtgcagagag	tggattgtca	gtggactgct	cagttacaaa	tgggacatct	aacacacaca	60
cacacacaca	cacacacaca	cacacacaca	cacccaagg	cttagagacc	attgcagaag	120
agaagagttt	atgggaaatc	ttggagaaaa	cattggatgg	tttgagagaa	tggttaggag	180
atcagactag	ctagtccagg	aagcagtga	ggggggcggg	gttagaagat	gaggtcagaa	240
gacaggggtg	agggcattgt	ccgacagaac	cattgctgt			279

&lt;210&gt; 90

&lt;211&gt; 398

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 90

ccaccaaccc	agaaatttga	caaaggggtt	gaatgttga	ctttgcgtcc	ttccccggca	60
gtggatgtac	tgttttgagc	cctgtgtgga	acttctgaac	ttcgtgctgt	aactttcaga	120
actcttagac	atgggtgtgc	tcaactgaact	ctaggggtctg	tgtgctagat	gctgccaacg	180
ctgtattcag	gacctgaagt	gagtaccctg	gtggatccag	accaatccag	tgtgagacta	240
ctgaagaaca	tctgttgcca	gaacggccac	accaaacaga	tggagtggcc	cagcacttag	300
cttcttaaat	aacatcggaa	ccattcagcc	agcgagtctg	tgtttgcttt	ttgttaaatt	360
gtccgccgaa	tctaaattcc	tccaaaaggc	ttgtgacc			398

&lt;210&gt; 91

&lt;211&gt; 279

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 91

gttggtactt	cagttgtctt	cggcggaat	tcttaaaactg	catcctgagt	gagggagctt	60
tggcgagaaa	gcaagaccca	gtggtagaca	gattagcatt	actgtacagc	ttctttgggt	120
gttcgaggaa	gcccggctgg	accatagtgg	ccacggcggg	gaggtaggcg	tggacagggc	180
tgaccagtcc	aagtttaagga	cgttcgggtc	catgttaacc	ctgccttgta	cgtccagcat	240
cgtaagaaaa	aacacttgag	aacccgaaga	ggagatgga			279

&lt;210&gt; 92

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 92

aaaaagtttt	accaaaaacct	tttattgact	tttataaatt	agatagtatt	tcaaagttta	60
tgtagaatcg	tattcttttga	aactgtactt	agcagagcag	aagaggcctg	ctgacgctag	120
cacgctctgc	aatgaatcat	gtggcaccga	gtctacgcca	aggcccccca	gaaactttat	180
tccatagatg	ggcagatggg	tcccaaagt	acactacaga	actacaaatc	gactcttaaa	240
attaaaacgg	gactttacaa	gcattctaga	agactcaaac	ttgaagcaat	ttttggaaaa	300
taaatgtaca	gagaaaagat	cttgaagcta	ctgaacagag	aaccctcatt	aaccgagcaa	360
atacatccta	tggagcttcc	gaggagtaca	cagacagacc	g		401

&lt;210&gt; 93

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; mouse

&lt;400&gt; 93

```

ccactgacct tcccagaagg tgacagccgg cggcgggatgt tgtcaaggag ccgagatagt      60
ccagcagtgct ctccgtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg      120
atgagaagtc accacagtga tctcacatct tgcgagatta tcctgatgga gatggagtcc      180
catgatgcag cctggccttt cctagagcct gtgaaccttc gcttggtgag tggataccga      240
cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg      300
tacactagct cagaagagtt tgcagctgat gctctgctg      339

```

```

<210> 94
<211> 55
<212> DNA
<213> mouse

```

```

<400> 94
ggggtgtggg caacttggat aacctcagct gcttccatct ggctgacatc tttgg      55

```

```

<210> 95
<211> 186
<212> DNA
<213> mouse

```

```

<400> 95
ggactctggc ttcttggggc tgcggccgac ctccgttggat cccgctctga ggcgggcgcg      60
gcgggggcccc agaaacaaga agcggggctg gaggaggctc gccgaggagc cgctgggggtt      120
agaggtcgac cagttccttg aagacgtccg gctacaggag cgcacgaccg gtggcttgtt      180
ggcaga      186

```

```

<210> 96
<211> 244
<212> DNA
<213> mouse

```

```

<400> 96
ggtgacaaa acoccttctg ccccttcccc agagactctg acttgaccct ctttccaatt      60
ccctctcccc aaggccatgg attatgaagc ccctctgtaa gatggtgagc caggggcccc      120
aagagggcac gaggcacacc ctgatcactg tctcaggcct ttgtgggcac tgactcgacc      180
ctggcccacc tcacgcccc aggccagttg gcaactgggtg gctcttgagg gctcttacgc      240
cctt      244

```

```

<210> 97
<211> 116
<212> DNA
<213> mouse

```

```

<220>
<221> unsure
<222> (11)...(11)

```

```

<221> unsure
<222> (13)...(13)

```

```

<221> unsure
<222> (41)...(41)

```

```

<400> 97
acccggctctg ngnactgccc gccttctggg gcttccttta naggatacag tcttttacct      60
atctaggact cctgccaccc tgactgctga cttacagcta tgagggtccg gcttct      116

```

<210> 98  
 <211> 307  
 <212> DNA  
 <213> mouse

<400> 98  
 ccccgggcca tctgtcgcca taccggggccc gtgcaagctt ttgcaggttt tagaagatgg 60  
 cgaattcatg acacctgtga tccaggacaa cccctcaggc tggggtcctt gtgccgttcc 120  
 tgagcaattt cgggatatgc cctaccagcc attcagcaaa ggagatcggc tgggaaagggt 180  
 tgcagactgg acagggggcca cataccagga caagaggtag acaacaagt attcctctca 240  
 gttcgggtggg gggagtcagt atgcatattt ccatgaggag gatgagacaa gctttccagc 300  
 tgggtgg 307

<210> 99  
 <211> 360  
 <212> DNA  
 <213> mouse

<220>  
 <221> misc\_feature  
 <222> (1)...(360)  
 <223> n = A,T,C or G

<400> 99  
 ccttgggtgca ccagctccag cctcaggact tcctcctcct ggccctgaca gccagctct 60  
 tgtcccagca gaatccagt acaggaagga gtttctgagg caggggagga ggcttctcca 120  
 tgggaaccag acagccttgc ttcactgtat aagtgcctg atcacacgca gaatgaagtg 180  
 ccaggttgct cagaagcaca aagggtgtgg ctactggccc taacctatga ctacgtgggt 240  
 ctaaccaaag actctagaac tctgggggtgg gggagaaaaca atgtgttctg tgctccagaa 300  
 ccttnggctt cctggcccat atggatgggc ttggcaagga acctacctct tctctaaggt 360

<210> 100  
 <211> 257  
 <212> DNA  
 <213> mouse

<400> 100  
 tgccgcgctg agaggggggg cgcaccacc agcgccacca ccaccaccgc cgcgcgcgcc 60  
 ggggtgggggtg ggagggggcg gagccaccgc taccgcccgc gcctcccggg tgggcgcctt 120  
 tctccttaga cgcggggcgac ccaggacgag ggcttcatca ctgtaaatgg ttgcaagccg 180  
 acaaagctgc acctcctgaa aaagacggac agcccatcgc gtgagctgta gaaatttgtg 240  
 gacgcatttc tatcgggt 257

<210> 101  
 <211> 203  
 <212> DNA  
 <213> mouse

<400> 101  
 ccaaagtgcc cattgtgatt caagacgata gccttccac gggggccctt ccacagatcc 60  
 gcatoctcaa gagggcccacc agcaacgggtg tggtcagcag ccccaactcc accagcaggc 120  
 cagcccttcc tgtcaagtcc ctacacagc gggaggcaga gtatgcagag gctcggagac 180  
 ggatocctagg cagtgcacgc cct 203

<210> 102  
 <211> 300

<212> DNA  
<213> mouse

<400> 102

agtacagaga	cctcggctgc	agcttaaaacc	tcggacagtg	gcaacgcccc	tcaatcaagt	60
agccaacccc	aactcagcca	tctttggggg	agccaggccc	agagaggaag	tggttcagaa	120
ggagcaagaa	tgagcttagg	ttgggagggg	atggggcgctg	ggggagctgg	agcaagacca	180
cggcctggtg	gcagccggtc	gccctacagg	ccccattccc	gcctggcact	gtcctcctta	240
cagcggaaac	acagagcttg	tgagtgcattg	tcagctgtta	acaagtgggt	tctagtacat	300

<210> 103  
<211> 370  
<212> DNA  
<213> mouse

<220>

<400> 103

cagcaactgt	ttcaggagct	gcacggtgta	cgctgtctga	ctgatgcgct	ggaactaaca	60
ctgggctggg	cccccaaaga	aaaccctccg	gtgatgcttc	cagcccaaga	gacggagagg	120
gccatggaga	tcctcaaagt	gctctttaat	atcacctttg	actctgtcaa	gaggggaagt	180
gatgaggaag	atgctgccct	ttaccggtag	ctggggactc	ttctgcggca	ctgcgtgatg	240
gttgaagctg	ctggggaccg	cacagaggag	ttccacggcc	acacggtgaa	tctcctgggg	300
aacttgcccc	tcaagtgttt	ggatgtgctt	ctggccctgg	agctccacga	aggatcctta	360
gagtcagtgg						370

<210> 104  
<211> 423  
<212> DNA  
<213> mouse

<400> 104

tttcccagcc	tggtggagca	gccgactggc	gagtgtgcc	actgtccgct	gcttcccagc	60
tcctaccttg	cctgtcttct	ctctcctggg	aagatgttcc	tggtggggct	gacgggaggc	120
atcgccctag	gcaagagctc	cgctcatccag	gtattccaac	agctgggctg	tgctgtaatc	180
gacgtggaog	tcattgcgcg	gcacgttgct	cagccagggg	atcctgcccc	ccggcggtata	240
gtagaggcct	ttggcactga	agtcttgctg	gagaatggcg	acatcgaccg	caaggctctc	300
ggagacctga	tcttcaacca	gcctgaccgt	cgccagctgc	tcaactccat	taccaccctc	360
gagatccgca	aggaaatgat	gaaggagacc	ttcaagtact	tctccgaggt	accgatagct	420
gat						423

<210> 105  
<211> 117  
<212> DNA  
<213> mouse

<400> 105

agcttggtgc	tggtcatatt	taaactgata	aagactcttc	ataggagctg	agggtagcaa	60
gcccgcgtcg	gtgactgggg	tctcacacag	gttcagcact	tgagacatag	tgaggtg	117

<210> 106  
<211> 133  
<212> DNA  
<213> mouse

<400> 106

```

ttttttttttt aaaataccac cattttccaat cccaaaagaa catggcactt gtttgtttct      60
tccccttctc attcattoca gactttcaag tgttttcttc aatactgagg ctttctcctg      120
cagctctgggt ctg                                                         133

```

```

<210> 107
<211> 217
<212> DNA
<213> mouse

```

```

<220>
<221> unsure
<222> (1)...(1)

```

```

<221> unsure
<222> (11)...(11)

```

```

<221> unsure
<222> (18)...(23)

```

```

<221> unsure
<222> (34)...(34)

```

```

<221> unsure
<222> (37)...(38)

```

```

<221> unsure
<222> (40)...(42)

```

```

<221> unsure
<222> (50)...(52)

```

```

<221> unsure
<222> (55)...(58)

```

```

<221> unsure
<222> (152)...(152)

```

```

<221> unsure
<222> (155)...(155)

```

```

<221> unsure
<222> (165)...(165)

```

```

<400> 107

```

```

ntttttttttg ngcgcacnnn nnnngnnnncg cccnggnngn nnagcctacn nncannnnngt      60
tttcttctcc aggctgaaga cctgaacgtc aagttggaag gggagccttc catgcggaaa      120
ccaaagcagc ggccgcggcc ggagcccctc ancancccca ccaangeggg cactttcctc      180
gcccctcctg tctactccaa catcaccctc taccaga,                               217

```

```

<210> 108
<211> 346
<212> DNA
<213> mouse

```

```

<220>

```

```

<400> 108

```

```

gggcatagaa ggcattctga aaagaatact tatttgaatt gaaggaagat gaagaggcct      60
gcaggaaggc tcagaagaca ggagtgtttt acctctttca tgacctggat cctttgctcc      120
aggcgtcagg acatcgatac ctgggtgccc ggcttagccg agcagagttg gaaggggtgc      180
tgggtaagtt cggacaggat tcgcaaagaa ttgaagattc ggtgctggtt ggggtgctccg      240
agcagcagga agcatggttt gctttggatc taggtctgaa gagtgcctcc tccagccgtg      300
gacaagtatc gctgctccag cagcttgact gctgtaaaga ggatct      346

```

<210> 109  
 <211> 242  
 <212> DNA  
 <213> mouse

```

<400> 109
ccacattgtc cacaactgga aggcacgatg gttcatcctt cggcagaaca cgctcctgta      60
ttacaagcta gaggggtggc ggcgagtaac cccgcccaag gggaggattg tccttgatgg      120
ctgcaccatc acctgcccct gcctggagta tgaaaaccgg ccgctcctca ttaactgaa      180
gaccggaact tccactgagt acttcctgga agcctgttct cgagaggaga gagactcctg      240
gg                                     242

```

<210> 110  
 <211> 310  
 <212> DNA  
 <213> mouse

<220>  
 <221> misc\_feature  
 <222> (1)...(310)  
 <223> n = A,T,C or G

```

<400> 110
ccccgccggg aatccagggt gtagctggtg gattcgccctc cggagagtga cgcgcagact      60
cggctccccc gccgcccgcc ctccctgccg cctcgccgcg gtctcccttg ctccctgaga      120
tcgctgagcg ctgagcagcg gccggggaga ggaggccttg ggcgacgggg cgcggagagg      180
gagggcgggc gggcantggg ggcgcccgcg atctctatat ggcgacgggt ctgtcgggtc      240
tggtgttccg gctgtcgcgc tcggccggnc ggccggttcc tatggggtct tctgcaaagg      300
ggttgaccgg                                     310

```

<210> 111  
 <211> 228  
 <212> DNA  
 <213> mouse

```

<400> 111
ttctttttta acatttgggt gttttttttt ttactctttt tttcttttcc ttctttttct      60
gccctcaacc ccccaactcc tttggatga agtactttta acatttata ttcattgtta      120
cactttaaat tttgtaagga aaactctgat atttcattcc tcctgaacca ctaatgttag      180
aatatttttc taagaatcag tcaacatgta tactcttaat agtgaatt      228

```

<210> 112  
 <211> 292  
 <212> DNA  
 <213> mouse

```

<400> 112
gtgggggtccc agacttgcca accaaagggc cattcctggg atatggttct ggcttcagct      60
ctgggtggcat ggactatggg atgggtgggt gcaaggaggc tgggaccgag tctcgcttca      120
aacagtggac ctcaatgatg gaagggtgac catctgtggc cacacaagaa gccaccatgc      180

```



acaaaaacgg cgctatagtg gcccctggta agaccogagg aggttcacca tacaaccagt 240  
 ttgatataat cccaggtgac aactgggtg gccatcggg tctgtctggt ga 292

<210> 113  
 <211> 255  
 <212> DNA  
 <213> mouse

<220>

<400> 113  
 ttagatgact taggacttta atgttttcca tgcagtogat tgaaaacact gatacatgaa 60  
 caaccagaaa aagacctcag caatgtatag acctggaata tatagtgttg ccttgggttaa 120  
 actacaagaa cagccacgtg atcacagttt gaggggtggaa ggcaggggtg tgactgagtt 180  
 ttgtttaacg gcctaaccga aaagcaaaga atcaaccatt tcttctactt gtggcaagaa 240  
 acgagagtca tgggtg 255

<210> 114  
 <211> 197  
 <212> DNA  
 <213> mouse

<400> 114  
 gaccacatg tgaacagccg cgtgtatgtc acactgctct gtgtgtgatt tottcacgtg 60  
 tgcattgtgc ctcttgggtc ttccacttat tgcctcgttc gtaagaaacc aaccataagg 120  
 tgccaaggag gttttattcc tttttttttt aaagatgaca aatgtacaga tgtagtaga 180  
 gatgttaatg tacagat 197

<210> 115  
 <211> 205  
 <212> DNA  
 <213> mouse

<400> 115  
 aaaaatttc aaaaaacagc aaaacaaaat tgatacaatc aaaaaacaa cactataacc 60  
 aacatagggtg aaaacagcca aacacataat gtacaatctg gtgttccagg aaaaacatct 120  
 gtcataatac tgggtatatac atatatactt tttcactcaa tatattatga caatatatat 180  
 ttaaaatttt gttatagaca aaaaa 205

<210> 116  
 <211> 202  
 <212> DNA  
 <213> mouse

<220>

<400> 116  
 cctccctcat cctotacttc ccttttctct cctgcttgat tttctcattc cagaccctta 60  
 tgcacacaca cacacacaca cacacacaca caggaacaca cgcacacaca cacacacagc 120  
 cacacacaca ctgtccatcc atagttactt atttagtttt ccattcctag agagatctaa 180  
 tcatccctta gtcagtgcct aa 202

<210> 117  
 <211> 240  
 <212> DNA  
 <213> mouse

<400> 117  
 ccgccaggag agggagataca cagccagtga tgtggaccac cggatggctg ttgctgctgc 60  
 cgcttctgct gtgtgaagga gcgcaagccc tggagtgtga cagctgcgtg cagaaggcgg 120  
 acgatggatg cgctccgcac aggatgaaga cagtcaaatg tgggtcccggg gtggacgtct 180  
 gtaccgagggc cgtgggagcg gtagagacca tccacgggca attctctgtg gcggtgcggg 240

<210> 118  
 <211> 527  
 <212> DNA  
 <213> Human

<400> 118  
 ccgtcagttc agaaggataa gagaaagaaa gttaagcaac tacaggaaat ggctttggga 60  
 gttccaatat cagtctatct tttattcaac gcaatgacag cactgaccga agaggcagcc 120  
 gtgactgtaa cacctccaat cacagcccag caaggtaact ggacagttaa caaacagaa 180  
 gctcacaaca tagaaggacc catagccttg aagtctctac acctttgcct ggaagatcat 240  
 aacagttaact gcatcaacgg tgctttgtgca ttccaccatg agctagagaa agccatctgc 300  
 aggtgtttta ctggttatac tggagaaagg tgtgagcact tgactttaac ttcatatgct 360  
 gtggattctt atgaaaaata cattgcaatt gggattgggt ttggattact attaagtggt 420  
 tttcttgtaa ttttttactg ctatataaga aagaggtgtc taaaattgaa atcgcccttac 480  
 aatgtctggt ctggagaaag acgaccactg tgaggccttt gtgaaga 527

<210> 119  
 <211> 655  
 <212> DNA  
 <213> Rat

<400> 119  
 atggcgcgcc ccgcgccctg gtggtggctg cggccgctgg cggcgctcgc cctggcgctg 60  
 gcgctggtcc ggggtgccctc agcccggggc gggcagatgc cgcgccccgc agagcgcggg 120  
 cccccagtac ggctcttcac cgaggaggag ctggcccgtc acagcgcgga ggaggaggat 180  
 caaccatct acttggcagt gaagggagtg gtgttcgatg tcacctctgg gaaggagttt 240  
 tatggacgtg gagcccccta caacgccttg gccgggaagg actcgagcag aggtgtggcc 300  
 aagatgtcgc tggatcctgc agacctcact catgacattt ctggtctcac tgccaaggag 360  
 ctggaagccc tcgatgacat cttcagcaag gtgtacaaag ccaaataccc cattgttggc 420  
 tacacggccc gcaggatcct caacgaggat ggcagcccca acctggactt caagcctgaa 480  
 gaccagcccc attttgacat aaaggacgag ttctaattgtc tagctgagaa gctggttcta 540  
 gggagaggtg aggggacagg agttaaattgt cccacggaac aagcagggga agcctctgag 600  
 tgcctctgcat ctgaataaaa ctgatattta actgggaaaa aaaaaaaaaa aaaaa 655

<210> 120  
 <211> 176  
 <212> PRT  
 <213> Rat

<400> 120  
 Met Val Pro Cys Phe Leu Leu Ser Leu Leu Leu Val Arg Pro Ala  
 1 5 10 15  
 Pro Val Val Ala Tyr Ser Val Ser Leu Pro Ala Ser Phe Leu Glu Glu  
 20 25 30  
 Val Ala Gly Ser Gly Glu Ala Glu Gly Ser Ser Ala Ser Pro Ser  
 35 40 45  
 Leu Leu Pro Pro Arg Thr Pro Ala Phe Ser Pro Thr Pro Gly Arg Thr  
 50 55 60  
 Gln Pro Thr Ala Pro Val Gly Pro Val Pro Pro Thr Asn Leu Leu Asp  
 65 70 75 80

Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val  
                   85                  90                  95  
 Gly Ser Leu Thr Phe Leu Ile Met Phe Ile Val Cys Ala Ala Leu Ile  
                   100                  105                  110  
 Thr Arg Gln Lys His Lys Ala Thr Ala Tyr Tyr Pro Ser Ser Phe Pro  
                   115                  120                  125  
 Glu Lys Lys Tyr Val Asp Gln Arg Asp Arg Ala Gly Gly Pro His Ala  
                   130                  135                  140  
 Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Gln Glu Glu Gly  
 145                  150                  155                  160  
 Leu Asp Phe Phe Gln Gln Leu Gln Ala Asp Ile Leu Ala Cys Tyr Ser  
                   165                  170                  175

<210> 121  
 <211> 116  
 <212> PRT  
 <213> Rat

<400> 121  
 Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr  
   1                  5                  10                  15  
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met  
                   20                  25                  30  
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp  
                   35                  40                  45  
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr  
                   50                  55                  60  
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr  
 65                  70                  75                  80  
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro  
                   85                  90                  95  
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln  
                   100                  105                  110  
 Gln Lys Gln Gln  
                   115

<210> 122  
 <211> 64  
 <212> PRT  
 <213> Human

<400> 122  
 Met Asn Leu Leu Ile Gly Ser Ile Ile Leu Ser Ser Phe Leu Val Leu  
   1                  5                  10                  15  
 Ser Asp Gly Asp Thr Thr Ala Ser Pro Ser Ser Met Ser Ser Ser  
                   20                  25                  30  
 Val Leu Asn His Ile Ser Ser Ser Ser Ser Val Trp His Leu Phe  
                   35                  40                  45  
 Asp Ile Cys Asp Ser Ser Lys Trp Asn Ala Tyr Cys Gln Val Trp Gly  
                   50                  55                  60

<210> 123  
 <211> 68  
 <212> PRT  
 <213> Human

<400> 123

Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg  
 1 5 10 15  
 Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly  
 20 25 30  
 Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr  
 35 40 45  
 Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe  
 50 55 60  
 Ser Cys Leu Leu  
 65

<210> 124  
 <211> 110  
 <212> PRT  
 <213> mouse

<400> 124  
 Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly  
 1 5 10 15  
 Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro  
 20 25 30  
 Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser  
 35 40 45  
 Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr  
 50 55 60  
 Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys  
 65 70 75 80  
 Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp  
 85 90 95  
 Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His  
 100 105 110

<210> 125  
 <211> 330  
 <212> PRT  
 <213> mouse

<400> 125  
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu  
 1 5 10 15  
 Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg  
 20 25 30  
 Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe  
 35 40 45  
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys  
 50 55 60  
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser  
 65 70 75 80  
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His  
 85 90 95  
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr  
 100 105 110  
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu  
 115 120 125  
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu  
 130 135 140  
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala

```

145          150          155          160
Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
          165          170          175
Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
          180          185          190
Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
          195          200          205
Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp
          210          215          220
Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp
225          230          235          240
Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro
          245          250          255
Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro
          260          265          270
Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
          275          280          285
Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
          290          295          300
Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
305          310          315          320
Pro Ser Trp Thr Val Ser Met Asp Thr Gln
          325          330

```

```

<210> 126
<211> 37
<212> PRT
<213> Rat

```

```

<400> 126
Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
1          5          10          15
Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
          20          25          30
Arg Ala Asp Val Leu
          35

```

```

<210> 127
<211> 42
<212> PRT
<213> mouse

```

```

<400> 127
Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
1          5          10          15
Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
          20          25          30
Ser Leu His Thr Met Ser Ala Gly Phe Pro
          35          40

```

```

<210> 128
<211> 253
<212> PRT
<213> mouse

```

```

<400> 128
Met Met Tyr Trp Ile Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe

```

```

      1           5           10           15
Thr Asp Ile Phe Ile Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp
      20           25           30
Gly Trp Glu Gly Pro His His His His Leu Ala Ser Gly Ser His
      35           40           45
Lys Pro Leu Pro Leu Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe
      50           55           60
Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala
      65           70           75           80
Ser Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser Arg His Glu
      85           90           95
Lys Glu Ile Asp Ala Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu
      100           105           110
Thr Met Leu Ser Phe Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala
      115           120           125
Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu
      130           135           140
Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val
      145           150           155           160
Pro Thr Tyr Gln Asp Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg
      165           170           175
Arg Pro Pro Ile Gly Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr
      180           185           190
Glu Asp Glu Cys Trp Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val
      195           200           205
Arg Pro Arg Glu Lys Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val
      210           215           220
Lys Arg Lys Pro Leu Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val
      225           230           235           240
Arg Thr Arg Lys Lys Ala Met Pro Ser Asp Met Asp Ser
      245           250

```

```

<210> 129
<211> 40
<212> PRT
<213> mouse

```

```

      <400> 129
Met Lys Ala Met Ala Leu Ser Leu Gly Ala Ser Pro Val Leu Ala Phe
      1           5           10           15
Leu Leu Ser Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly
      20           25           30
Ser Lys Val Pro Gln Phe Leu Asn
      35           40

```

```

<210> 130
<211> 87
<212> PRT
<213> mouse

```

```

      <400> 130
Met Ile Ala Val Thr Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg
      1           5           10           15
Ile Ser Thr Ala Ala Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg
      20           25           30
Ser Asn Ile Arg Val Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu
      35           40           45

```

Val Val Ile Ile Leu Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp  
 50 55 60  
 Leu Thr Lys Ile Gly Glu Cys His Val Gln Asp Ser Ile Gly Ser Met  
 65 70 75 80  
 Gly Leu Gly Gln Gly Gln Pro  
 85

<210> 131  
 <211> 70  
 <212> PRT  
 <213> mouse

<400> 131  
 Met Phe Gly Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys  
 1 5 10 15  
 Val Cys Val Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro  
 20 25 30  
 Cys Gly Cys Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu  
 35 40 45  
 Ser Leu His Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro  
 50 55 60  
 Gly Leu Ser Leu Ile Ser  
 65 70

<210> 132  
 <211> 63  
 <212> PRT  
 <213> mouse

<400> 132  
 Met Trp Leu Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala  
 1 5 10 15  
 Phe Val Thr Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met  
 20 25 30  
 Ser Leu His Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly  
 35 40 45  
 Val Pro Leu Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu  
 50 55 60

<210> 133  
 <211> 39  
 <212> PRT  
 <213> mouse

<400> 133  
 Met Asp Asn Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala  
 1 5 10 15  
 Ile Ser Val Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe  
 20 25 30  
 Ser Lys Asp Leu Glu Val Thr  
 35

<210> 134  
 <211> 90  
 <212> PRT  
 <213> Rat

<400> 134  
 Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val  
 1 5 10 15  
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala  
 20 25 30  
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val  
 35 40 45  
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val  
 50 55 60  
 Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe  
 65 70 75 80  
 Ala Gly Glu Val Leu Gly Ile Cys His Ser  
 85 90

<210> 135  
 <211> 193  
 <212> PRT  
 <213> Rat

<400> 135  
 Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys  
 1 5 10 15  
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser  
 20 25 30  
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile  
 35 40 45  
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu  
 50 55 60  
 Tyr His Ser Phe Val Ser Ser Val Phe Thr Leu Phe Met Ser Arg Thr  
 65 70 75 80  
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro  
 85 90 95  
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His  
 100 105 110  
 Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met  
 115 120 125  
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met  
 130 135 140  
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu  
 145 150 155 160  
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu  
 165 170 175  
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Met  
 180 185 190  
 Ser

<210> 136  
 <211> 106  
 <212> PRT  
 <213> Rat

<400> 136  
 Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala  
 1 5 10 15  
 Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser  
 20 25 30



Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln  
 35 40 45  
 Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala  
 50 55 60  
 Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val  
 65 70 75 80  
 Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr  
 85 90 95  
 Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys  
 100 105

&lt;210&gt; 137

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 137

Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu  
 1 5 10 15  
 Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu  
 20 25 30  
 Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala  
 35 40 45  
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly  
 50 55 60  
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser  
 65 70 75 80  
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp  
 85 90 95  
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala  
 100 105 110  
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser  
 115 120 125  
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu  
 130 135 140  
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys  
 145 150 155 160  
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala  
 165 170 175  
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys  
 180 185 190  
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys  
 195 200 205  
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile  
 210 215 220  
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu  
 225 230 235 240  
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly  
 245 250 255  
 Lys Lys Glu Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp  
 260 265 270  
 Ile Thr Gly Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser  
 275 280 285

&lt;210&gt; 138

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 138

```

Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
 1      5      10      15
Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
 20      25      30
Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
 35      40      45
Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly
 50      55      60
Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
 65      70      75      80
Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
 85      90      95
Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
 100     105     110
Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
 115     120     125
His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro
 130     135     140
Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
 145     150     155     160
Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
 165     170     175
Lys Phe Asp Lys Ile Leu Met Asn Glu Gly His Tyr Asn Ala Ser
 180     185     190
Ser Gly Lys Phe Val Cys
 195

```

&lt;210&gt; 139

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 139

```

Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1      5      10      15
Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20      25      30
Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35      40      45
Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50      55      60
Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65      70      75      80
Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85      90      95
Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
 100     105     110
Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
 115     120     125
Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
 130     135     140
Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
 145     150     155     160
Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu

```

```

                165                170                175
Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
                180                185                190
Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Met Lys
                195                200                205
Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
                210                215                220
Glu Asp Thr Glu Phe Leu Gln Pro Gly
225                230

```

```

<210> 140
<211> 38
<212> PRT
<213> Human

```

```

<400> 140
Met Gly Leu Ala Leu Cys Leu Ala Ser Ala Gly Ile Ser Gly Ser Arg
 1          5          10          15
Ser Ala Phe Leu Gly Val Pro Arg Pro Arg Pro Thr Leu Ile Lys Leu
                20          25          30
Ile Asp Thr Val Asp Leu
          35

```

```

<210> 141
<211> 322
<212> PRT
<213> mouse

```

```

<400> 141
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1          5          10          15
Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
                20          25          30
Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
          35          40          45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
          50          55          60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
          65          70          75          80
Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
          85          90          95
Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
          100          105          110
Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
          115          120          125
Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
          130          135          140
Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
          145          150          155          160
Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
          165          170          175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
          180          185          190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
          195          200          205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
          210          215          220

```

```

Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225          230          235          240
Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
          245          250          255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
          260          265          270
Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
          275          280          285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
          290          295          300
Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305          310          315          320
Gln Gly

```

```

<210> 142
<211> 312
<212> PRT
<213> mouse

```

```

<400> 142
Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
1          5          10          15
Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
          20          25          30
Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
          35          40          45
Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
50          55          60
Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
65          70          75          80
Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly
          85          90          95
Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val
100          105          110
Lys Ile Ser Glu Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys
115          120          125
Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu
130          135          140
Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His
145          150          155          160
Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe
          165          170          175
Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala
180          185          190
Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp
195          200          205
Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met
210          215          220
Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys
225          230          235          240
Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu
          245          250          255
Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly
          260          265          270
Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser
275          280          285

```

Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu  
 290 295 300  
 Lys Thr Arg Met Ala Leu Arg Lys  
 305 310

<210> 143  
 <211> 163  
 <212> PRT  
 <213> Rat

<400> 143  
 Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr  
 1 5 10 15  
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe  
 20 25 30  
 Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala  
 35 40 45  
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn  
 50 55 60  
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val  
 65 70 75 80  
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu  
 85 90 95  
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr  
 100 105 110  
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys  
 115 120 125  
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser  
 130 135 140  
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg  
 145 150 155 160  
 Trp Lys Asn

<210> 144  
 <211> 330  
 <212> PRT  
 <213> Rat

<400> 144  
 Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg  
 1 5 10 15  
 Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu  
 20 25 30  
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp  
 35 40 45  
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala  
 50 55 60  
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr  
 65 70 75 80  
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln  
 85 90 95  
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu  
 100 105 110  
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys  
 115 120 125  
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val

130		135		140
Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe				
145		150		155
Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys				160
		165		170
Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln				175
		180		185
Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu				190
		195		200
Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp				205
		210		215
Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg				220
225		230		235
Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe				240
		245		250
Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu				255
		260		265
Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr				270
		275		280
Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala				285
		290		295
Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys				300
305		310		315
His Arg Lys Ala Phe Leu Pro Phe Leu Phe				320
		325		330

&lt;210&gt; 145

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 145

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly				
1		5		10
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser				15
		20		25
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu				30
		35		40
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr				45
		50		55
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val				60
65		70		75
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile				80
		85		90
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr				95
		100		105
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn				110
		115		120
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg				125
		130		135
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu				140
145		150		155
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser				160
		165		170
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe				175
		180		185
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp				190

```

      195      200      205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
  210      215      220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
  225      230      235      240
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
      245      250      255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
      260      265      270
Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
      275      280      285
Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
      290      295      300

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<210> 146
<211> 61
<212> PRT
<213> Rat

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```

      <400> 146
Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
  1      5      10      15
His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
      20      25      30
Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
      35      40      45
Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
      50      55      60

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<210> 147
<211> 105
<212> PRT
<213> Rat

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```

      <400> 147
Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
  1      5      10      15
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
      20      25      30
Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
      35      40      45
Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile
      50      55      60
Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
      65      70      75      80
Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
      85      90      95
Glu Arg Gly Gln His Gly Pro Lys Gly
      100      105

```

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<210> 148
<211> 210
<212> PRT
<213> Rat

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```

      <400> 148
Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val

```

```

      1           5           10           15
Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu
      20           25           30
Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser
      35           40           45
Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile
      50           55           60
Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His
      65           70           75           80
Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser
      85           90           95
Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr
      100          105          110
His Leu Gln Thr Pro Leu Gln Ala Trp Arg Thr Arg Ala Lys Leu Pro
      115          120          125
Pro Gly Gly Thr Glu Ala Val Pro Gly Arg Pro Gly Ala Gln Gln Asp
      130          135          140
Ala Cys His Leu Leu Tyr Trp Thr Tyr Asn Gly Val Ser Ser Ile Pro
      145          150          155          160
Cys His Arg Gly Gly Leu Ser His Val Pro Ser Glu Val Pro Ala Glu
      165          170          175
Lys Ser Pro Val Leu Ile Leu His Ala Ala Pro Pro Phe Lys Thr Pro
      180          185          190
Val Asn Pro Trp Ala Arg Thr Val Val Gly Phe Phe Pro Ser Ser Pro
      195          200          205
Ser Leu
      210

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<210> 149
<211> 301
<212> PRT
<213> Rat

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```

      <400> 149
Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
      1           5           10           15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
      20           25           30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
      35           40           45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
      50           55           60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
      65           70           75           80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
      85           90           95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
      100          105          110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
      115          120          125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
      130          135          140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
      145          150          155          160
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
      165          170          175
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe

```



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      180      185      190
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
      195      200      205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
      210      215      220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
      225      230      235
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
      245      250      255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
      260      265      270
Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
      275      280      285
Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
      290      295      300

```

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<210> 150
<211> 80
<212> PRT
<213> Human

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      <400> 150
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
      5      10      15
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
      20      25      30
Phe Gln Asp Thr Lys Val Tyr Cys Thr Arg Glu Ser Asn Pro His Cys
      35      40      45
Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala Phe Cys Lys Ala
      50      55      60
Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys His Pro Gly Lys Cys
      65      70      75      80

```

```

<210> 151
<211> 27
<212> PRT
<213> mouse

```

```

      <400> 151
Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
      5      10      15
Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
      20      25

```

```

<210> 152
<211> 86
<212> PRT
<213> mouse

```

```

      <400> 152
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
      5      10      15
Cys Val Phe Trp Asp Phe Ile Phe Ile Phe Phe Asn Val Leu Ser
      20      25      30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
      35      40      45
Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly

```

50                      55                      60  
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp  
 65                      70                      75                      80  
 Leu Leu Ser Phe Pro Pro  
                     85

<210> 153  
 <211> 72  
 <212> PRT  
 <213> mouse

<400> 153  
 Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu  
 1                      5                      10                      15  
 Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu  
                     20                      25                      30  
 Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg  
                     35                      40                      45  
 Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met  
                     50                      55                      60  
 Ala Phe Ser Ile Leu Phe Ile Gln  
 65                      70

<210> 154  
 <211> 169  
 <212> PRT  
 <213> mouse

<400> 154  
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly  
 1                      5                      10                      15  
 Ser Arg Leu Pro Arg Val Ile Ser Gln Ser Val Cys Arg Ala Arg  
                     20                      25                      30  
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly  
                     35                      40                      45  
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln  
                     50                      55                      60  
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu  
 65                      70                      75                      80  
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr  
                     85                      90                      95  
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly  
                     100                      105                      110  
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe  
                     115                      120                      125  
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu  
                     130                      135                      140  
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu  
 145                      150                      155                      160  
 Gly Glu Met Pro Pro Glu Asp Gly Met  
                     165

<210> 155  
 <211> 61  
 <212> PRT  
 <213> mouse

<400> 155  
 Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile  
 1 5 10 15  
 Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val  
 20 25 30  
 Thr Val Thr Gln Met Arg Thr Ile Ile Thr Met Asp Gln Leu Arg  
 35 40 45  
 Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser  
 50 55 60

<210> 156  
 <211> 131  
 <212> PRT  
 <213> mouse

<400> 156  
 Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala  
 1 5 10 15  
 Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg  
 20 25 30  
 Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln  
 35 40 45  
 Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala  
 50 55 60  
 Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr  
 65 70 75 80  
 Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg  
 85 90 95  
 Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu  
 100 105 110  
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser  
 115 120 125  
 Leu Arg Arg  
 130

<210> 157  
 <211> 133  
 <212> PRT  
 <213> mouse

<400> 157  
 Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys  
 1 5 10 15  
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro  
 20 25 30  
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 35 40 45  
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Glu His Val  
 50 55 60  
 Gln Gly Thr Gly Ala Arg Ser Thr Ala Cys Thr Leu Ser Cys Arg Ala  
 65 70 75 80  
 Pro Asn Ala Ser Ser Ser Gly Thr Met Pro Gly Thr Arg Ser Ala Gly  
 85 90 95  
 Ser Thr Lys Asn Arg Val Asp Asp His Gly Lys Lys Asn Ser Arg Pro  
 100 105 110  
 Val Glu Arg Leu Gln Gln Arg Thr Leu Gln Ile Lys Ile Lys Ala Leu  
 115 120 125

Ser Phe Ser Gln Ala  
130

<210> 158  
<211> 78  
<212> PRT  
<213> mouse

<400> 158  
Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys  
1 5 10 15  
Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser  
20 25 30  
Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu  
35 40 45  
Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His  
50 55 60  
Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val  
65 70 75

<210> 159  
<211> 206  
<212> PRT  
<213> mouse

<400> 159  
Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile  
1 5 10 15  
Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu  
20 25 30  
Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser  
35 40 45  
Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly  
50 55 60  
Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser  
65 70 75 80  
Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys  
85 90 95  
Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn  
100 105 110  
Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser  
115 120 125  
Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln  
130 135 140  
Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val  
145 150 155 160  
Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser  
165 170 175  
His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg  
180 185 190  
Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser  
195 200 205

<210> 160  
<211> 169  
<212> PRT  
<213> mouse

<400> 160  
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly  
 1 5 10 15  
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg  
 20 25 30  
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly  
 35 40 45  
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln  
 50 55 60  
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu  
 65 70 75 80  
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr  
 85 90 95  
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly  
 100 105 110  
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe  
 115 120 125  
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu  
 130 135 140  
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu  
 145 150 155 160  
 Gly Glu Met Pro Pro Glu Asp Gly Met  
 165

<210> 161  
 <211> 114  
 <212> PRT  
 <213> mouse

<400> 161  
 Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu  
 1 5 10 15  
 Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp  
 20 25 30  
 Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Arg Leu  
 35 40 45  
 Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile  
 50 55 60  
 His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys  
 65 70 75 80  
 Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys  
 85 90 95  
 Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val  
 100 105 110  
 Ser Leu

<210> 162  
 <211> 46  
 <212> PRT  
 <213> mouse

<400> 162  
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys  
 1 5 10 15  
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu



<210> 166  
 <211> 75  
 <212> PRT  
 <213> mouse

<400> 166  
 Lys Thr Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp  
 1 5 10 15  
 Phe Met Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro  
 20 25 30  
 Phe Pro Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys  
 35 40 45  
 Gln Trp Glu Gly Ser Thr Met Thr His Thr His Thr His Thr His Ile  
 50 55 60  
 His Ile His Thr Pro Pro Arg Gln Cys Gln Ser  
 65 70 75

<210> 167  
 <211> 52  
 <212> PRT  
 <213> mouse

<400> 167  
 Val Arg Ser Leu Glu Gln Leu Gly Leu Phe Ser Val Asp Phe Met Val  
 1 5 10 15  
 Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro Leu  
 20 25 30  
 Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp Glu  
 35 40 45  
 Gly Ser Thr Met  
 50

<210> 168  
 <211> 119  
 <212> PRT  
 <213> Rat

<400> 168  
 Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val  
 1 5 10 15  
 Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu  
 20 25 30  
 Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser  
 35 40 45  
 Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile  
 50 55 60  
 Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His  
 65 70 75 80  
 Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser  
 85 90 95  
 Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr  
 100 105 110  
 His Leu Gln Thr Pro Leu Gln  
 115

<210> 169  
 <211> 104

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;220&gt;

&lt;400&gt; 169

```

Leu Val Pro Lys Ser Ala Arg Ala Ser Leu Leu Cys Cys Gly Pro Lys
 1          5          10          15
Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu
          20          25          30
Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Xaa Ile Xaa
          35          40          45
Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile
          50          55          60
Tyr Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly
65          70          75          80
Leu Tyr Leu Leu Xaa Gly Gly Phe Ser Phe Cys Gln Val Arg Leu Asn
          85          90          95
Lys Arg Lys Glu Tyr Met Val Arg
          100

```

&lt;210&gt; 170

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (27)...(27)

&lt;221&gt; UNSURE

&lt;222&gt; (104)...(104)

&lt;221&gt; UNSURE

&lt;222&gt; (118)...(118)

&lt;400&gt; 170

```

Met Arg Pro Gly Ala Asp Trp Ala Ala Val Cys Ala Leu Trp Pro Ser
 1          5          10          15
Trp Arg Pro Ser Cys Ser Leu Pro Ser Ser Xaa Arg Ile Gln Pro Asp
          20          25          30
Glu Leu Trp Leu Tyr Arg Asn Pro Tyr Val Lys Ala Glu Tyr Phe Pro
          35          40          45
Thr Gly Pro Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile
          50          55          60
Phe Phe Ala Lys Phe Leu Arg Lys Ala Asp Ala Asp Arg Gln Arg Ala
65          70          75          80
Ser Leu Pro Arg Cys Gln Pro Cys Pro Ser Ala Lys Trp Cys Leu Tyr
          85          90          95
Gln His His Lys Thr Asp Ser Xaa Gln Gly His Ala Gln Ile Ala Ser
          100          105          110
Thr Glu Cys Ser Pro Xaa Gly Ile Ala His Ser
          115          120

```

&lt;210&gt; 171

&lt;211&gt; 75



&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 171

```

Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
 1          5          10          15
Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
          20          25          30
Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
          35          40          45
Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
          50          55          60
Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
65          70          75

```

&lt;210&gt; 172

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 172

```

Lys Thr Ser Tyr His Tyr His Thr Asn Val Glu Glu Leu Thr Ile Pro
 1          5          10          15
Glu Thr Arg Asn Asn Leu Tyr Ile Ser Ile Ser Trp Leu Trp Cys Leu
          20          25          30
Val Leu Val Leu Leu Ser Thr Met Ile Leu Asn Lys His Gly Trp Met
          35          40          45
Lys Ala Asn Ala Tyr Ser Leu Val Pro Ser Ile Ile Tyr Ser Pro Ser
          50          55          60
Tyr Leu Lys Leu Leu Leu Arg Leu Tyr Lys Leu Gln Ile Cys Cys
65          70          75

```

&lt;210&gt; 173

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;220&gt;

&lt;400&gt; 173

```

Leu Arg Gly Arg Gly Arg Gly Val Cys Ser Gln Glu Ser Phe Gly Gly
 1          5          10          15
Cys Cys Val Ser Gly Leu Ile Ala Met Gly Thr Lys Ala Gln Val Glu
          20          25          30
Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu
          35          40          45
Ala Leu Gly Ser Val Thr Val His Ser Ser Glu Pro Glu Val Arg Ile
          50          55          60
Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser
65          70          75          80
Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu
          85          90          95
Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr
          100          105          110
Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr
          115          120          125
Gly Thr Tyr Thr Cys Met
130

```

<210> 174  
 <211> 137  
 <212> PRT  
 <213> Human

<400> 174

Ala Trp Ser Arg Pro Arg Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala  
 1 5 10 15  
 Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe  
 20 25 30  
 Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly  
 35 40 45  
 Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile  
 50 55 60  
 Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr  
 65 70 75 80  
 Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn  
 85 90 95  
 Ile Lys Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser  
 100 105 110  
 Ala Leu Val Ile Leu Gly Gly Ala Leu Ser Pro Val Pro Val Leu Gly  
 115 120 125  
 Ile Arg Ala Gly Leu Gly Thr Cys Pro  
 130 135

<210> 175  
 <211> 43  
 <212> PRT  
 <213> Human

<400> 175

Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys  
 1 5 10 15  
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu  
 20 25 30  
 Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn  
 35 40

<210> 176  
 <211> 63  
 <212> PRT  
 <213> Rat

<400> 176

Pro Asn Thr Arg Pro Arg Arg His Thr Ala Cys Arg Val Ser Ile Ser  
 1 5 10 15  
 Val Phe Tyr Met Leu His Thr Glu Leu Lys Lys Cys Trp Phe Phe Leu  
 20 25 30  
 Phe Cys Phe Ser Leu Phe Leu Trp Phe Cys Phe Trp Phe Cys Phe Leu  
 35 40 45  
 Leu Pro Arg Phe Asp Tyr Leu Pro Met Pro Ser Thr Arg Pro Arg  
 50 55 60

<210> 177  
 <211> 52  
 <212> PRT

&lt;213&gt; mouse

&lt;400&gt; 177

```

Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
1      5      10      15
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
20      25      30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
35      40      45
Gly Ala Gln Gly
50

```

&lt;210&gt; 178

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 178

```

Val Ser Pro Arg Pro Thr Tyr Pro Ser Thr Ala Ser Ser Met Ala Ala
1      5      10      15
Phe Leu Val Thr Gly Phe Phe Phe Ser Leu Phe Val Val Leu Gly Met
20      25      30
Glu Pro Arg Ala Leu Phe Arg Pro Asp Lys Ala Leu Pro Leu Ser Cys
35      40      45
Ala Lys Pro Thr Ser Leu Cys Val Gln Ser Ser Phe Leu Gly
50      55      60

```

&lt;210&gt; 179

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 179

```

Ala Ser Arg Thr Ala Val Met Ser Leu Cys Arg Cys Gln Gln Gly Ser
1      5      10      15
Arg Ser Arg Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly
20      25      30
Gly Thr Leu Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu
35      40      45
Trp Pro Ser Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Arg Arg Thr
50      55      60
Leu Gly Met Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys
65      70      75      80
Tyr Ser Phe Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu
85      90      95
His Gly Phe Ser Ala His Lys Gly His Val Ala Gln Arg Gly Gln Val
100      105      110
Pro Ser Arg Lys Asn Leu His Phe Gly Cys Val
115      120

```

&lt;210&gt; 180

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (5)...(5)

&lt;400&gt; 180

Ala	Arg	Arg	Arg	Xaa	Arg	Trp	Arg	Arg	Gly	Cys	Cys	Trp	Leu	Ile	Gly
1				5					10					15	
Thr	Gly	Leu	Arg	Ala	Ala	Thr	Trp	Thr	Val	Leu	Cys	Ser	Pro	Asn	Ser
			20					25					30		
Ser	Leu	Val	Val	Ala	Arg	His	Thr	Lys	Ser	Phe	Pro	Pro	Lys	Lys	Pro
		35					40					45			
Leu	Gln	Ala	Leu	Thr	Met	Ser	Ile	Met	Asp	His	Ser	Pro	Thr	Thr	Gly
	50					55					60				
Val	Val	Thr	Val	Ile	Val	Ile	Leu	Ile	Ala	Ile	Ala	Ala	Leu	Gly	Gly
	65				70					75				80	
Leu	Ile	Leu	Gly	Cys	Trp	Cys	Tyr	Leu	Arg	Leu	Gln	Arg	Ile	Ser	Gln
				85					90					95	
Ser	Glu	Asp	Glu	Glu	Ser	Ile	Val	Gly	Asp	Gly	Glu	Thr	Lys	Glu	Pro
			100					105					110		
Phe	Tyr	Trp	Cys	Ser	Thr	Leu	Leu								
		115					120								

&lt;210&gt; 181

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 181

Lys	Gly	Pro	Glu	Val	Ser	Cys	Cys	Ile	Lys	Tyr	Phe	Ile	Phe	Gly	Phe
1				5					10					15	
Asn	Val	Ile	Phe	Trp	Phe	Leu	Gly	Ile	Thr	Phe	Leu	Gly	Ile	Gly	Leu
			20					25					30		
Trp	Ala	Trp	Asn	Glu	Lys	Gly	Val	Leu	Ser	Asn	Ile	Ser	Ser	Ile	Thr
		35					40					45			
Asp	Leu	Gly	Gly	Phe	Asp	Pro	Val	Trp	Leu	Phe	Leu				
	50					55					60				

&lt;210&gt; 182

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;220&gt;

&lt;400&gt; 182

Lys	Pro	Thr	Val	Gly	Ser	Ala	Glu	Val	Ala	Ile	Ala	Val	Phe	Leu	Val
1				5					10					15	
Ile	Cys	Ile	Ile	Val	Val	Leu	Thr	Ile	Leu	Gly	Tyr	Cys	Phe	Phe	Lys
			20					25					30		
Asn	Gln	Arg	Lys	Glu	Phe	His	Ser	Pro	Leu	His	His	Pro	Pro	Pro	Thr
		35					40					45			
Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu	Asp	Thr	Glu	His	Leu	Val
	50					55					60				
Tyr	Asn	His	Thr	Thr	Gln	Pro	Leu								
	65				70										

&lt;210&gt; 183

&lt;211&gt; 771

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;220&gt;

&lt;400&gt; 183

```

Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu Leu
 1      5      10      15
Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg Ile
 20      25      30
Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu Thr
 35      40      45
Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr Phe
 50      55      60
Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp Ile
 65      70      75      80
Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu Ser Ala Leu Ser His
 85      90      95
Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln Trp
100      105      110
Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala Arg
115      120      125
Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr Pro
130      135      140
Ser Lys Asn Phe Thr Cys Gln Gly Pro Val Asp Val Thr Ile Gln Ala
145      150      155      160
Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr Cys
165      170      175
Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly Phe
180      185      190
Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Thr Ser Asn Pro
195      200      205
Cys Lys His Gly Gly Thr Cys His Leu Lys Pro Arg Arg Glu Thr Trp
210      215      220
Ile Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly Glu Ser Cys Asp Ile
225      230      235      240
Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr Cys
245      250      255
Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr Thr
260      265      270
Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu Asn
275      280      285
Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe Lys
290      295      300
Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His Cys Asp Ile Asp Phe
305      310      315      320
Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr Asp
325      330      335
Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu Gly Tyr Ser Gly Leu
340      345      350
Phe Cys Glu Phe Ser Pro Pro Met Val Phe Leu Arg Thr Ser Pro Cys
355      360      365
Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Ile Arg Val Asn
370      375      380
Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu Gly Glu Lys Cys Glu
385      390      395      400

```

Lys Leu Val Ser Val Ser Ile Leu Val Asn Lys Glu Ser Tyr Leu Gln  
 405 410 415  
 Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile  
 420 425 430  
 Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp  
 435 440 445  
 His Ile Ala Val Glu Ser Ile Glu Gly Ile Arg Ala Ser Tyr Asp Thr  
 450 455 460  
 Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn Asp  
 465 470 475 480  
 Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu Asp Ser Ser Leu Ser  
 485 490 495  
 Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile Thr Asn Leu Ser Lys  
 500 505 510  
 Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met Pro  
 515 520 525  
 Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn Gly  
 530 535 540  
 Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu Leu  
 545 550 555 560  
 Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly Ile Leu Pro Gly Cys  
 565 570 575  
 Glu Pro Cys His Lys Lys Val Cys Ala His Gly Thr Cys Gln Pro Ser  
 580 585 590  
 Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu Gly Trp Met Gly Pro  
 595 600 605  
 Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys Val  
 610 615 620  
 His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys Cys  
 625 630 635 640  
 Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu Phe  
 645 650 655  
 Asn Pro Leu Pro Gly Asp Gln Val Gln Ala Arg Glu Val Gln Ala Leu  
 660 665 670  
 Trp Ala Arg Ala Ala Leu Leu Trp Met Gln Gln Trp Ile His Arg Gly  
 675 680 685  
 Gln Leu Thr Gln Arg Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp Tyr  
 690 695 700  
 Tyr Gln Ser Ser Arg Val Arg Cys Leu Ser Asn Asp

&lt;210&gt; 184

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 184

Asp Gly Ser Leu Trp Leu Gln Ala Thr Gln Pro Asp Asp Ala Gly His  
 1 5 10 15  
 Tyr Thr Cys Val Pro Ser Asn Gly Phe Leu His Pro Pro Ser Ala Ser  
 20 25 30  
 Ala Tyr Leu Thr Val Leu Tyr Pro Ala Gln Val Thr Val Met Pro Pro  
 35 40 45  
 Glu Thr Pro Leu Pro Thr Gly Met Arg Gly Val Ile Arg Cys Pro Val  
 50 55 60  
 Arg Ala Asn Pro Pro Leu Phe Val Thr Trp Thr Lys Asp Gly Gln  
 65 70 75 80  
 Ala Leu Gln Leu Asp Lys Phe Pro Gly Trp Ser Leu Gly Pro Glu Gly

```

      85      90      95
Ser Leu Ile Ile Ala Leu Gly Asn Glu Asp Ala Leu Gly Glu Tyr Ser
      100      105      110
Cys Thr Pro Tyr Asn Ser Leu Gly Thr Ala Gly Pro Ser Pro Val Thr
      115      120      125
Arg Val Leu Leu Lys Ala Pro Pro Ala Phe Ile Asp Gln Pro Lys Glu
      130      135      140
Glu Tyr Phe Gln Glu Val Gly Arg Glu Leu Leu Ile Pro Cys Ser Ala
      145      150      155      160
Arg Gly Asp Pro Pro Ile Val Ser Trp Ala Lys Val Gly Arg Gly
      165      170      175
Leu Gln Gly Gln Ala Gln Val Asp Ser Asn Asn Ser Leu Val Leu Arg
      180      185      190
Pro Leu Thr Lys Glu Ala Gln Gly Arg Trp Glu Cys Ser Ala Ser Asn
      195      200      205
Ala Val Ala Arg Val Thr Thr Ser Thr Asn Val Tyr Val Leu Gly Thr
      210      215      220
Ser Pro His Val Val Thr Asn Val Ser Val Val Pro Leu Pro Lys Gly
      225      230      235      240
Ala Asn Val Ser Trp Glu Pro Gly Phe Asp Gly Gly Tyr Leu Gln Arg
      245      250      255
Phe Ser Val Trp Tyr Thr Pro Leu Ala Lys Arg Pro Asp Arg Ala His
      260      265      270
His Asp Trp Val Ser Leu Ala Val Pro Ile Gly Ala Thr His Leu Leu
      275      280      285
Val Pro Gly Leu Gln Ala His Ala Gln Tyr Gln Phe Ser Val Leu Ala
      290      295      300
Gln Asn Lys Leu Gly Ser Gly Pro Phe Ser Glu Ile Val Leu Ser Ile
      305      310      315      320
Pro Glu Gly Leu Pro Thr Thr Pro Ala Ala Pro Gly Leu Pro Ala Thr
      325      330      335
Arg Ser Arg Val
      340

```

```

<210> 185
<211> 536
<212> PRT
<213> mouse

```

```

      <400> 185
Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
      5      10      15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
      20      25      30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
      35      40      45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
      50      55      60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
      65      70      75      80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
      85      90      95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
      100      105      110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
      115      120      125
Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp

```

130	135	140
Leu Lys Pro Ala Asn Ile	Leu Leu Asp Ala His	Tyr Gln Met Ser Arg
145	150	155
Phe Leu Asp Phe Gly Leu	Ala Lys Cys Asn Gly	Met Ser His Ser His
165	170	175
Asp Leu Ser Met Asp Gly	Leu Phe Gly Thr Ile	Gly Tyr Leu Pro Pro
180	185	190
Glu Arg Ile Arg Glu Lys	Ser Arg Leu Phe Asp Thr	Lys His Asp Val
195	200	205
Tyr Ser Phe Ala Ile Val	Ile Trp Gly Val Leu Thr	Gln Asn Asn Pro
210	215	220
Phe Ala Asp Glu Lys Asn	Ile Leu His Ile Met Met	Lys Val Val Lys
225	230	235
Gly His Arg Pro Glu Leu	Pro Pro Ile Cys Arg Pro	Arg Pro Arg Ala
245	250	255
Cys Ala Ser Leu Ile Gly	Leu Met Gln Arg Cys Trp	His Ala Asp Pro
260	265	270
Gln Val Arg Pro Thr Phe	Gln Glu Ile Thr Ser Glu	Thr Glu Asp Leu
275	280	285
Cys Glu Lys Pro Asp Glu	Glu Val Lys Asp Leu Ala	His Glu Pro Gly
290	295	300
Glu Lys Ser Ser Leu Glu	Ser Lys Ser Glu Ala Arg	Pro Glu Ser Ser
305	310	315
Arg Leu Lys Arg Ala Ser	Ala Pro Pro Phe Asp Asn	Asp Cys Ser Leu
325	330	335
Ser Glu Leu Leu Ser Gln	Leu Asp Ser Gly Ile Phe	Pro Arg Leu Leu
340	345	350
Lys Gly Pro Glu Glu Leu	Ser Arg Ser Ser Ser Glu	Cys Lys Leu Pro
355	360	365
Ser Ser Ser Ser Gly Lys	Arg Leu Ser Gly Val Ser	Ser Val Asp Ser
370	375	380
Ala Phe Ser Ser Arg Gly	Ser Leu Ser Leu Ser Phe	Glu Arg Glu Ala
385	390	395
Ser Thr Gly Asp Leu Gly	Pro Thr Asp Ile Gln Lys	Lys Lys Leu Val
405	410	415
Asp Ala Ile Ile Ser Gly	Asp Thr Ser Arg Leu Met	Lys Ile Leu Gln
420	425	430
Pro Gln Asp Val Asp Leu	Val Leu Asp Ser Ser Ala	Ser Leu Leu His
435	440	445
Leu Ala Val Glu Ala Gly	Gln Glu Glu Cys Val Lys	Trp Leu Leu Leu
450	455	460
Asn Asn Ala Asn Pro Asn	Leu Thr Asn Arg Lys Gly	Ser Thr Pro Leu
465	470	475
His Met Ala Val Glu Arg	Lys Gly Arg Gly Ile Val	Glu Leu Leu Leu
485	490	495
Ala Arg Lys Thr Ser Val	Asn Ala Lys Asp Glu Asp	Gln Trp Thr Ala
500	505	510
Leu His Phe Ala Ala Gln	Asn Gly Asp Glu Gly Gln	His Lys Ala Ala
515	520	525
Ala Arg Glu Glu Cys Phe	Cys Gln	
530	535	

<210> 186  
 <211> 337  
 <212> PRT  
 <213> Rat



&lt;220&gt;

&lt;400&gt; 186

```

Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp
 1      5      10      15
Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile
      20      25      30
Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr
      35      40      45
Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly
      50      55      60
Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr
      65      70      75      80
Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp
      85      90      95
Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn
      100     105     110
Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu
      115     120     125
Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
      130     135     140
Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys
      145     150     155     160
Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser Cys Gln
      165     170     175
Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro Leu Gln
      180     185     190
Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Val
      195     200     205
Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met Cys Pro
      210     215     220
Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Phe Arg
      225     230     235     240
Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln
      245     250     255
Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile
      260     265     270
Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro
      275     280     285
Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp
      290     295     300
Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe
      305     310     315     320
Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro
      325     330     335
Phe

```

&lt;210&gt; 187

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 187

```

Met Ala Leu Gly Val Leu Ile Ala Val Cys Leu Leu Phe Lys Ala Met
 1      5      10      15

```

Lys Ala Ala Leu Ser Glu Glu Ala Glu Val Ile Pro Pro Ser Thr Ala  
 20 25 30  
 Gln Gln Ser Asn Trp Thr Phe Asn Asn Thr Glu Ala Asp Tyr Ile Glu  
 35 40 45  
 Glu Pro Val Ala Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn  
 50 55 60  
 Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln  
 65 70 75 80  
 Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His  
 85 90 95  
 Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile Ala  
 100 105 110  
 Ile Gly Ile Gly Val Gly Leu Leu Ile Ser Ala Phe Leu Ala Val Phe  
 115 120 125  
 Tyr Cys Tyr Ile Arg Lys Arg Cys Ile Asn Leu Lys Ser Pro Tyr Ile  
 130 135 140  
 Ile Cys Ser Gly Gly Ser Pro Leu  
 145 150

<210> 188  
 <211> 118  
 <212> PRT  
 <213> Rat

<220>

<400> 188  
 Leu Val Pro Gln Phe Gly Thr Arg Ile Arg Tyr Thr Ala Tyr Asp Arg  
 1 5 10 15  
 Ala Tyr Asn Arg Ala Ser Cys Lys Phe Ile Val Lys Val Gln Val Arg  
 20 25 30  
 Arg Cys Pro Ile Leu Lys Pro Pro Gln His Gly Tyr Leu Thr Cys Ser  
 35 40 45  
 Ser Ala Gly Asp Asn Tyr Gly Ala Ile Cys Glu Tyr His Cys Asp Gly  
 50 55 60  
 Gly Tyr Glu Arg Gln Gly Thr Pro Ser Arg Val Cys Gln Ser Ser Arg  
 65 70 75 80  
 Gln Trp Ser Gly Ser Pro Pro Val Cys Thr Pro Met Lys Ile Asn Val  
 85 90 95  
 Asn Val Asn Ser Ala Ala Gly Leu Leu Asp Gln Phe Tyr Glu Lys Gln  
 100 105 110  
 Arg Leu Leu Ile Val Ser  
 115

<210> 189  
 <211> 299  
 <212> PRT  
 <213> Human

<220>

<400> 189  
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30  
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu

```

          35          40          45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
  50          55          60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
  65          70          75          80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
          85          90          95
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
          100          105          110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
          115          120          125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
          130          135          140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
          145          150          155          160
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
          165          170          175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
          180          185          190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
          195          200          205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
          210          215          220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
          225          230          235          240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
          245          250          255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
          260          265          270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
          275          280          285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
          290          295

```

```

<210> 190
<211> 91
<212> PRT
<213> Human

```

```

          <400> 190
Gln Pro Thr Val Phe Trp Pro Lys Thr Ser Ala Lys Lys Gly Asn Trp
  1          5          10          15
Val Leu Arg Leu Gly Leu Ser Asn Pro Asp Arg Pro Ala Arg Gln Asn
          20          25          30
Asn Trp Phe Leu Pro Ala Ser Arg Glu Ile Pro Glu His Ser Ala Leu
          35          40          45
Thr Arg Tyr Pro Ala Gln Ile Arg Gly Cys Trp Pro His Arg Leu Thr
          50          55          60
Lys Pro Gln Thr Cys Leu Pro Gln Ala Arg Ser Tyr Leu Ser His Glu
          65          70          75          80
Val Thr Gln Ala Thr Arg Thr Cys Pro Gly Gly
          85          90

```

```

<210> 191
<211> 89
<212> PRT
<213> mouse

```

<400> 191  
 Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu Asp  
 1 5 10 15  
 Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly Lys  
 20 25 30  
 Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr Ala  
 35 40 45  
 Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr Pro  
 50 55 60  
 Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr Pro  
 65 70 75 80  
 Cys Gln Pro Gly Gln Arg Val Glu Val  
 85

<210> 192  
 <211> 299  
 <212> PRT  
 <213> mouse

<220>

<400> 192  
 Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp  
 1 5 10 15  
 Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His  
 20 25 30  
 Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr  
 35 40 45  
 Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys  
 50 55 60  
 Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg  
 65 70 75 80  
 Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu  
 85 90 95  
 Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr  
 100 105 110  
 Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys  
 115 120 125  
 Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln  
 130 135 140  
 Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln  
 145 150 155 160  
 Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly  
 165 170 175  
 Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly  
 180 185 190  
 Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys  
 195 200 205  
 Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro  
 210 215 220  
 Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg  
 225 230 235 240  
 Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp  
 245 250 255  
 Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly

```

                260                265                270
Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
                275                280                285
Pro Gln His Ser Ser Ser Lys Ala Met Lys His
                290                295

```

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<210> 193
<211> 314
<212> PRT
<213> mouse

```

```

<220>

```

```

                <400> 193
Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn Ile Asp
 1      5      10      15
Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met
                20      25      30
Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile
                35      40      45
Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr
                50      55      60
Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly
 65      70      75      80
Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His
                85      90      95
Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys
                100      105      110
Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln
                115      120      125
Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser
                130      135      140
Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr
 145      150      155      160
Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu
                165      170      175
Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly
                180      185      190
Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu
                195      200      205
Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly
                210      215      220
Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg
 225      230      235      240
Cys Val Asp Thr SerGln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala
                245      250      255
Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly
                260      265      270
Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln
                275      280      285
Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe
 290      295      300
Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
 305      310

```

```

<210> 194
<211> 109
<212> PRT

```

&lt;213&gt; mouse

&lt;400&gt; 194

```

Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
 1      5      10      15
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
 20      25      30
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
 35      40      45
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
 50      55      60
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
 65      70      75      80
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr
 85      90      95
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
100      105

```

&lt;210&gt; 195

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 195

```

Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1      5      10      15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
 20      25      30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
 35      40      45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
 50      55      60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
 65      70      75      80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
 85      90      95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
100      105      110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
115      120      125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
130      135      140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145      150      155      160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
165      170      175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
180      185      190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
195      200      205
Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu
210      215      220
His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe
225      230      235

```

&lt;210&gt; 196

&lt;211&gt; 154

<212> PRT  
<213> Human

<400> 196  
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met  
1 5 10 15  
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr  
20 25 30  
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala His Asn Ile  
35 40 45  
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His  
50 55 60  
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu  
65 70 75 80  
Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu  
85 90 95  
His Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile  
100 105 110  
Ala Ile Gly Ile Gly Val Gly Leu Leu Leu Ser Gly Phe Leu Val Ile  
115 120 125  
Phe Tyr Cys Tyr Ile Arg Lys Arg Cys Leu Lys Leu Lys Ser Pro Tyr  
130 135 140  
Asn Val Cys Ser Gly Glu Arg Arg Pro Leu  
145 150

<210> 197  
<211> 171  
<212> PRT  
<213> Rat

<400> 197  
Met Ala Arg Pro Ala Pro Trp Trp Trp Leu Arg Pro Leu Ala Ala Leu  
1 5 10 15  
Ala Leu Ala Leu Ala Leu Val Arg Val Pro Ser Ala Arg Ala Gly Gln  
20 25 30  
Met Pro Arg Pro Ala Glu Arg Gly Gly Pro Val Arg Leu Phe Thr Glu  
35 40 45  
Glu Glu Leu Ala Arg Tyr Ser Gly Glu Glu Glu Asp Gln Pro Ile Tyr  
50 55 60  
Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu Phe  
65 70 75 80  
Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Ala Gly Lys Asp Ser Ser  
85 90 95  
Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His Asp  
100 105 110  
Ile Ser Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Asp Ile Phe  
115 120 125  
Ser Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala Arg  
130 135 140  
Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro Glu  
145 150 155 160  
Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe  
165 170

<210> 198  
<211> 1399  
<212> DNA

## &lt;213&gt; Mouse

## &lt;400&gt; 198

ggcaaaagact	tgggcacag	asaacagcaa	agcagagctg	gctgcagcca	ttcactggcc	60
tcggggcgggc	gtgccacaga	ggcagttgaa	gtgaaagtga	aagagaaacg	ataagagAAC	120
ggagaccaca	gggtgctaagt	gaggggtgctc	acagaacccc	ctcttcagcc	agagatcact	180
agcaggggaa	ctgtggagaa	ggcagccagc	aaggaagagc	ctgagagtag	cctccatggg	240
cttgaggccc	agctggtatc	tgctgctctg	tttggctgtc	tctggggcag	cagggactga	300
ccctcccaca	gcgcccacca	cagcagaaag	acagcggcag	cccacggaca	tcactcttaga	360
ctgcttcttg	gtgacagaag	acaggcaccg	cggggctttt	gccagcagtg	gggacaggga	420
gagggccttg	cttgtgctga	agcagggtacc	agtgtctggat	gatggctccc	tggaaggcat	480
cacagatttc	caggggagca	ctgagaccaa	acaggattca	cctgttatct	ttgaggcctc	540
agtggacttg	gtacagattc	cccaggcaga	ggcgttgctc	catgtctgact	gcagcgggaa	600
ggcagtgacc	tgcgagatct	ccaagtattt	cctccaggcc	agacaagagg	ccacttttga	660
gaaagcacat	tggttcatca	gcaacatgca	ggtttctaga	ggtggcccca	gtgtctccat	720
ggtgatgaag	actctaagag	atgctgaagt	tggagctgtc	cggcacccta	cactgaacct	780
tgaggagcta	ctcagggtga	cagtgaagac	tcaagtggag	ttccagggtga	catcagagac	840
ccaaaccctg	aaccacctgc	tggggtcctc	tgtctccctg	cactgcagtt	tctccatggc	900
accagacctg	gacctcactg	gcgtggagtg	gcggctgcag	cataaaggca	gcggccagct	960
ggtgtacagc	tggaagacag	ggcaggggca	ggccaagcgc	aaggggcgta	cactggagcc	1020
agaggagctg	ctcagggtga	gaaacgcctc	tctcacctta	cccaacctca	ctctaaagga	1080
tgaggggacc	tacatctgcc	agatctccac	ctctctgtat	caagctcaac	agatcatgcc	1140
acttaacatc	ctggctcccc	caaaggtaca	actgcacttg	gcaacaagg	atcctctgcc	1200
ttccctcgtc	tgcagcattg	cgggtactta	tctcttggtg	gtgggagtg	cgtggattcg	1260
agaggagctg	ggtggaattc	cagcccaagt	ctctggtgcc	tcctctctca	gcctcaggca	1320
gagcacgatg	ggaacctaca	gcattttctt	cacgggtgatg	gctgaccag	gccccacagg	1380
tgccacttat	acctgccaa					1399

## &lt;210&gt; 199

## &lt;211&gt; 469

## &lt;212&gt; DNA

## &lt;213&gt; Rat

## &lt;400&gt; 199

ggggcgctgg	ccagtcagtg	cggagccttg	ggctgggcag	tttctgcaag	ctttgcccgc	60
cacggtgctc	ggagcgctgg	gcaccctggg	cagcgagttt	ctgcgggagt	gggagacaca	120
agatatgcga	gtgactctct	tcaagcttct	cctgctttgg	ttggtgttaa	gtctcctggg	180
catccagctg	gcgtgggggt	tctacgggaa	cacagtgacc	gggttgatc	accgtccagg	240
gaaatggcag	caaataaagc	tctcaaaact	cacagagaat	aaaggaaggc	agcaggagaa	300
gggtctccag	agatatcgct	gggtctgctg	gctcctgtgc	tgtaccttgc	tgctatccag	360
accccttagg	caactgcaga	gggcttgggt	tgggggactg	gagtaccatg	atgctcccag	420
ggtgagcctc	cactgccttc	agccttgctc	ccaacagcgt	caggtactg		469

## &lt;210&gt; 200

## &lt;211&gt; 529

## &lt;212&gt; DNA

## &lt;213&gt; Rat

## &lt;400&gt; 200

aaagcttcca	tcctcaacat	gccactagtg	acgacactct	tctacgcctg	cttctatcac	60
tacacggagt	ccgaggggac	cttcagcagt	ccagtcaacc	tgaagaaaac	attcaagatc	120
ccagacagac	agtatgtgct	gacagccttg	gctgcgcggg	ccaagcttag	agcctggaat	180
gatgtcgacg	ccttggttcc	cacaaagaac	tggttgggtt	acaccaagaa	gagagcaccc	240
attggcttcc	atcgagttgt	ggaatttttg	cacaagaaca	gtgcccctgt	ccagatattg	300
caggaatatg	tcaatctggt	ggaagatgtg	gacacaaagt	tgaacttagc	cactaagtcc	360
aagtgcctag	atggtgtcat	tgatacttgc	cgagacctga	aggatcgta	acagttgctt	420
gcatacagga	gcaaagtaga	taaaggatct	gctgaggaag	agaaaaatga	tgtcatcctc	480



agcagctcgc aaattcgatg gaagaactaa ggttcttttg ctaccaga 529

<210> 201  
<211> 1230  
<212> DNA  
<213> Rat

<400> 201  
aagaattcgg cagcaggcca tggctgggtg ggcggggggc gagctctcgg tcctgaaccc 60  
gctgctgctg ctgtggctgt tgctggccgc cgccttcctg ctgcactgc tgctgcagct 120  
ggcgcccgcc aggctgtac cgagctcgcg gctcttccag gacctcatcc gctacgggaa 180  
gaccaagcag tccggctcgc ggcgcccgcg cgtctgcagg gccttcgacg tccccagag 240  
gtacttttct cacttctacg tcgtctcagt gttatggaat ggctccctgc tctggttcct 300  
gtctcagttc ctgttctcgg gagcgccgtt tccaagctgg ctttgggctt tgctcagaac 360  
tcttggggtc acgcagtcc aagccctggg gatggagtcc aaggcttctc ggatacaagc 420  
aggcgagctg gctctgtcta cctctctagt gttgggtgtc ctctgggtcc atagtcttgc 480  
gagactcttc gagtgcctct acgtcagcgt cttctctaac acggccattc acgtcgtgca 540  
gtactgtttc gggctgggtc actatgtcct tggtggcctg accgtactga gccaaagtgc 600  
catgaatgac aagaacgtgt acgctctggg gaagaatcta ctgtacaag ctcggtggtt 660  
ccacatcttg ggaatgatga tgttcttctg gtcctctgcc catcagtata agtgccacgt 720  
cattctcagc aatctcagga gaaataagaa aggtgtggtc atccactgcc agcacagaat 780  
cccccttggg gactgggttc agtatgtgtc ttctgctaac tacctagcag agctgatgat 840  
ctacatctcc atggctgtca ccttcgggct ccacaacgta acctgggtggc tgggtgtgac 900  
ctatgtcttc ttcagccaag ccttctctgc gttcttcaac cacagggtct acaaaagcac 960  
atctgtctcc tacccaaagc ataggaaagc ttctctcccg ttcttgtttt gaacaggctt 1020  
tatggtgaag agcgagccc aggtgacagg ttcccttctc cgagacgctg agacaggctg 1080  
aagtacactt tctgcagctg ggcgccgcca ggctgctacc gagctgcgcg ctcttccagg 1140  
acctcatccg ctacgggaag accaagcagt ccggctcgcg gcgccccgcc gtctgcagcc 1200  
cgggggatcc actagtctca gagcgccgcc 1230

<210> 202  
<211> 778  
<212> DNA  
<213> Rat

<400> 202  
ctgcaggctg acactagtgg atccaaagat tcggcacgag ataaggcaca tttgcttcat 60  
aaaataaaaa aaaaggaaat ttacttagcc gcatgtcagt cacccaaatt ttgagtgtac 120  
aaatgaaatg gaaaacattt attacacaaa tttaattaca attctaggga ataaacatgc 180  
aaatcagatg gagctcaatc tgcaggcgct gatcctctcc ccctgggttg cagtctgtgc 240  
acctcctgga ttgcgccgag accaggcagt cagaggcctg gctcttgacg gcaggaggat 300  
cactgttgta aagaacagcg tcacatttag cgcactctgg gtagtagcag tttttaacac 360  
tttgcgcagg tgcctccctt cccccacccg cgctttgtta ggtctacctc tctaaatctc 420  
tgccttcttc gcacagtaag tgacctctcc atgacaaaag gccccagac agcagttata 480  
aatcaatgtg ttttgggttt gtttgtttgt ttgttttgtt ttaaagaaaa acccggccat 540  
gcttggtggc acttgccctt aatagtagcg cttggttagac agaggcaagc ggttctctgt 600  
aagtccaagg ccagcctggt ctacacagtg agaccgggtc taaaaaaca aacaacaaa 660  
aacaactcct attgaatcca ctacaggaag gggggggcgc gatcactgtc tgcaactaa 720  
agtgacttga gctcctgtca cagcctttcc agcaagggca agcttcttta ttagttat 778

<210> 203  
<211> 1123  
<212> DNA  
<213> Rat

<400> 203  
gggccccccc tcgagtcgac gktatcgata agcttgatat cgaattcctg caggtcgaca 60

ctagtggatc	caaagaattc	ggcacgagcc	tgaggcgact	acgggtgcggg	tgccgggtgc	120
cgggtgccta	cagcccccac	cagcttcccc	ggggagattc	tgccgatttg	tcacgagcca	180
tgctcaggag	gcagctcgtc	tggtggcacc	tgctggcttt	gcttttccctc	ccatttttgcc	240
tgtgtcaaga	tgaatacatg	gagttctccac	aagctggagg	actgccccca	gactgcagca	300
agtgttgcca	tggagattat	ggattccgtg	gttaccacagg	gccccctgga	cccccaggtc	360
ctoctggcat	tccaggaaac	catggaaaca	atggaaataa	cggagccact	ggccacgaag	420
gggccaaggg	tgagaaagga	gacaaaggcg	acctggggcc	tcgaggggaa	cgggggcagc	480
atggcccca	aggatagaag	ggataccacg	gggtgccacc	agagctgcag	attgcgttca	540
tggcttctct	agcgactcac	ttcagcaatc	agaacagtgg	cattatcttc	agcagtgttg	600
agaccaacat	tggaaacttc	ttcgatgtca	tgactggtag	atttggggcc	cccgtatcag	660
gcgtgtatct	cttcaccttc	agcatgatga	agcatgagga	cgtggaggaa	gtgtatgtgt	720
accttatgca	caatggtaac	acgggtgttca	gcatgtacag	ctatgaaaca	aagggaataa	780
cagatacatc	cagcaaccat	gcagtgcgtg	agttggccaa	aggagatgaa	gtctgtgctaa	840
gaatgggcaa	cggtgccctc	catggggacc	accagcgctt	ctctaccttc	gcaggctttc	900
tgctttttga	aactaagtga	tgagggaagtc	aggatagctc	catgctaagg	gcgattttgta	960
ggtgagctag	ggttggttagg	atctgagggg	tggtggagtt	gggcttctct	atggagttat	1020
taactgttac	attggtcaca	ctgctactca	ttctaattggc	ataccaatta	tgttggatag	1080
tttaggggct	aggaagaata	gaccacaagg	taatatcccc	aga		1123

<210> 204  
 <211> 434  
 <212> DNA  
 <213> Mouse

<400> 204						
accaccaagc	agatggaatg	ctggcacacc	catgcacctg	catggcgctca	cagggtggaag	60
attgttaaaa	aattgacatc	agaaatatct	acagaaatag	atacctgttt	gaataaagtt	120
agagatgaaa	tttttgctaa	acttcaaccg	aagcttagat	gcacattagg	tgacattggaa	180
agtcctgtgt	ttgcacttcc	tgtactgtta	aagcttgaa	cccatgttga	aagcctcttt	240
acatatctct	tttcttggaa	ttttgaaatg	tcccatgtgt	gacaccagta	ccaaaacagg	300
tgtgtgaaga	gtctgggtcac	ctttaccaat	attgttccct	agtggcatcc	actcaatgct	360
gcccattttg	gtccatgtaa	cagctgcaac	agtaaatcac	aaataagaaa	aatggtgttg	420
gaaagagcgt	cgcc					434

<210> 205  
 <211> 783  
 <212> DNA  
 <213> Mouse

<400> 205						
aattcgccac	gaggctagtc	gaatgtccgg	gctgcggacg	ctgctggggc	tggggctgct	60
ggttgcgggc	tcgcgcctgc	cacgggtcat	cagccagcag	agtgtgtgtc	gtgcaaggcc	120
catctggtgg	ggaacacagc	gcccgggctc	ggagaccatg	gcgggcgctg	cgggtgaagta	180
cttaagtcag	gaggaggctc	aggccgtgga	ccaagagctt	tttaacgagt	atcagttcag	240
cgtggatcaa	ctcatggagc	tggccgggtt	gagctgtgcc	acggctattg	ccaaggctta	300
tccccccacg	tctatgtcca	agagtcccc	gactgtcttg	gtcatctgtg	gccccggaaa	360
taacggaggg	gatgggctgg	tctgtgcgcg	acacctcaaa	ctttttggtt	accagccaac	420
tatctattac	ccaaaagac	ctaacaagcc	cctcttcaact	gggctagtga	ctcagtgtca	480
gaaaatggac	attcctttcc	ttggtgaaat	gccccagag	gatgggatgt	agagaaggga	540
aacctagcg	gaatccaacc	agacttactc	atctcaactga	cggcaccocaa	gaagtctgca	600
actcacttta	ctggccgata	tcattacctt	gggggtcgct	ttgtaccacc	tgctctagag	660
aagaagtacc	agctgaacct	gccatcttac	cctgacacag	agtgtgtcta	ccgtctacag	720
taagggaggt	gggtaggcag	gattctcaat	aaagacttgg	tactttctgt	cttgaaaaaa	780
aaa						783

<210> 206  
 <211> 480

<212> DNA  
<213> Mouse

<400> 206

aaatgaaaac	tcttgggarct	cgcgcgccctg	cagggtcgaca	ctagtggatc	caaagaattc	60
ggcacgagtt	aagggttttca	gacttttattt	catgggtattt	gacattgaca	catactgagt	120
tagtaacaag	ataccatgca	gctccctcta	gcctcggatc	accgaagcag	gaagaaggtc	180
agactgcccc	catcccagat	ttgcttagtt	tgtctcccaa	tgtgctggac	tttaaagaca	240
gggaatggag	aagcagatgg	atgcttcagt	ttcagtcatt	tttggctcta	tagtgatctc	300
tgcttccctg	tacctgtcct	tggtcggacc	ctgggcagta	actgtcactc	agatgaggac	360
gatcatcatt	acaatggacc	aactgaggga	tgccctcata	ttagaccaat	taaaagttgc	420
tgtgagttaa	accaggaatg	accgcacttc	cacatcagaa	atcaaacaaa	atcaatgggt	480

<210> 207  
<211> 501  
<212> DNA  
<213> Mouse

<400> 207

ctgcaggtcg	acactagtgg	atccaaagaa	ttcgggcacga	gaatcatggc	gccgtcgctg	60
tggaaggggc	ttgtagggtg	cgggcttttt	gccctagccc	acgctgcctt	ttcagctgcg	120
cagcatcggt	cttatatgcg	actaacagaa	aaggaagatg	aatcattacc	aatagatata	180
gttctttcaga	cacttctggc	ctttgcagtt	acctgttatg	gcatagtcca	tatcgcaggg	240
gagttcaaag	acatggatgc	cacttcagaa	ttaaagaata	agacatttga	taccttaagg	300
aatcacccat	ctttttatgt	gtttaaccat	cgtggtcgag	tgctgttccg	gccttcagat	360
gcaacaaatt	cttcaaacct	agatgcattg	tcctctaata	catcgttgaa	gttacgaaag	420
tttgactcac	tgccgccgtta	agctttttac	aaattaaata	acaggacaga	cacagaattg	480
agtattggag	tttgggggtg	a				501

<210> 208  
<211> 480  
<212> DNA  
<213> Mouse

<400> 208

ggcacgagga	agcctcttcc	catggaagca	cactctagga	gagagaaggc	ctctgggctc	60
cgcctggcct	ggcatttatga	atgcagtggg	gtcagtgtgt	ggtaggatgtg	tgtactgggt	120
tggttttcct	tttttagtttt	tttacttttt	agtttagttt	gttcttttcc	ttccccaata	180
aatcattctc	acatgcttcc	atgtttgttt	ctgagagggtg	ggggctcaaa	tgtagagaaa	240
gtaggcccca	gtccataagg	aggtgtgaac	acacccctt	actgcttacc	accattttga	300
caggaacgcc	caggaggggga	gggggagggg	aagagggtgag	ttctgcacag	tcggacattt	360
ctgttgcttt	tgcatgttta	atatagacgt	tcctgtcgat	ccttggggaga	tcattggcctt	420
cagatatgca	cacgaccttt	gaattgtgcc	tactaattat	agcagggggac	ttgggtaccc	480

<210> 209  
<211> 962  
<212> DNA  
<213> Mouse

<400> 209

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&lt;213&gt; Mouse

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&lt;212&gt; DNA

&lt;213&gt; Rat

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&lt;211&gt; 376

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 220

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&lt;210&gt; 221

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 221

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&lt;210&gt; 222

&lt;211&gt; 530

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 222

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&lt;210&gt; 223

&lt;211&gt; 550

&lt;212&gt; DNA

## &lt;213&gt; Mouse

## &lt;400&gt; 223

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## &lt;210&gt; 224

## &lt;211&gt; 470

## &lt;212&gt; DNA

## &lt;213&gt; Mouse

## &lt;400&gt; 224

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## &lt;210&gt; 225

## &lt;211&gt; 1752

## &lt;212&gt; DNA

## &lt;213&gt; Rat

## &lt;400&gt; 225

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 <211> 2165  
 <212> DNA  
 <213> Mouse

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 <211> 1348  
 <212> DNA  
 <213> Mouse

<220>  
 <221> unsure  
 <222> (644)... (644)

<400> 227

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 <211> 2296  
 <212> DNA  
 <213> Mouse

<220>  
 <221> unsure  
 <222> (2255)... (2255)

<400> 228

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&lt;210&gt; 229

&lt;211&gt; 1704

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;400&gt; 229

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&lt;210&gt; 230

&lt;211&gt; 2004

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 230

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&lt;210&gt; 231

&lt;211&gt; 1397

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 231

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&lt;210&gt; 232

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 232

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&lt;210&gt; 233

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 233

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 <213> Human

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 <212> DNA  
 <213> Mouse

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&lt;210&gt; 238

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 238

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&lt;210&gt; 239

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 239

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&lt;210&gt; 240

&lt;211&gt; 228

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 240

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 <213> Mouse

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 <213> Mouse

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 <213> Mouse

<400> 245

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 <213> Mouse

<400> 246

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&lt;210&gt; 247

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Rat

<400> 247

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&lt;211&gt; 1308

&lt;212&gt; DNA

&lt;213&gt; Rat

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&lt;211&gt; 1212

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 249

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&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 250

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 <213> Mouse

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 <213> Mouse

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&lt;210&gt; 257

&lt;211&gt; 3516

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 257

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 <213> Mouse

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&lt;210&gt; 259

&lt;211&gt; 1018

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 259

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&lt;210&gt; 260

&lt;211&gt; 2800

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 260

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&lt;210&gt; 261

&lt;211&gt; 1335

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 261

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caaggaaaaa	aaaaa					1335

<210> 262  
 <211> 1816  
 <212> DNA  
 <213> Mouse

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ctttgagtoc	aaggggcttc	ctgccgagct	gaaatccatc	ttcaaactca	gtgtccttat	180
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caaggacctt	gatgggcaac	tggactttga	agagtttgta	cattacctcc	aagatcatga	300
gaaaaaactg	aggctggtgt	tcaagagtct	ggacaaaaag	aatgatggtc	gaatcgatgc	360
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<210> 263  
 <211> 764  
 <212> DNA  
 <213> Mouse

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----------	------------	------------	------------	------------	------------	----

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cgggcgccat	cccccgccg	ccgcacgcac	aggccggcgc	cctccttgcc	tccctgctcc	180
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gaagatggtt	atcgtcacca	ccaagagcat	gtccagggtac	cggggccagg	agcactgcct	420
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agagacttca	gcagaggact	ttgcagatta	aaataaaagc	cctttctttc	tcacaagcat	600
aagacaaatt	atataattgt	atgaagctct	tcttaccagg	gtcagttttt	acattttata	660
gctgtgtgtg	aaaggcttcc	agatgtgaga	tccagctcgc	ctgcgcacca	gacttcatta	720
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<210> 264  
 <211> 1697  
 <212> DNA  
 <213> Mouse

<400> 264						
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aatgtagcgg	gctatgccag	ctttatggta	cctggctacc	tcctgggtgca	gtacttaaga	240
cgggaagaact	acctggagac	aggcaggggt	ctctgcttcc	ccctgggtgaa	agcctgtgtg	300
tttggcaatg	agcccaaggc	tcctgatgag	gttctcctgg	ctccgcggac	agagacagcg	360
gaatccaccc	cgtcttggca	ggtcctgaag	ctggcttctc	gtgcctcggg	tctccagggtg	420
tcctatctga	cttggggcat	actgcaggaa	agagtgtatga	ctggcagcta	cggggccaca	480
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cccatgtacc	ggtactcctt	tgccagtctg	tcaaatgtgc	ttageagctg	gtgccagtat	660
gaagcactta	agttcgtcag	cttccctacc	cagggtgctgg	cgaaggcctc	caagggtgatc	720
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gacagcttca	cctcaaattg	gcaggatgcc	ctgtttgcct	ataagatgtc	atcgggtgcag	960
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tgcttataaa	gccccacttt	catggaaatg	acagctgtgg	gtgtttgggt	agaggtgacc	1500
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tttgctcata	gcacgcaccc	ttgaggtac	caggcaccag	ctgggaagag	aatttaagag	1620
tcctgcagtt	cccctagggg	ccagtggaga	tggtgctgtg	ccagaaggga	caaaggcccc	1680
cagcccagtt	ggggccc					1697

<210> 265  
 <211> 159  
 <212> DNA  
 <213> Mouse

<220>

<400> 265  
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 aaccaaagca gcggccgcgg ccggagcccc tcatcatccc caccaaggcg ggcaactttca 120  
 tcgcccctcc tgtctactcc aacatcacc cttaccaga 159

<210> 266  
 <211> 292  
 <212> DNA  
 <213> Mouse

<400> 266  
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 ctggtggcat ggactatggt atggttgggt gcaaggaggc tgggaccgag tctcgcttca 120  
 aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc 180  
 acaaaaacgg cgctatagtg gccctggta agacccgagg aggttcacca tacaaccagt 240  
 ttgatataat ccaggtgac aactgggtg gccatacggg tcctgctggt ga 292

<210> 267  
 <211> 339  
 <212> DNA  
 <213> Mouse

<400> 267  
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 ccagcagtgct ctcggtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg 120  
 atgagaagtc accacagtga tctcacattt tgcgagatta tcctgatgga gatggagtcc 180  
 catgatgcag cctggccttt cctagagcct gtgaaccctc gcttgggtgag tggataccga 240  
 cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg 300  
 tacactagct cagaagagtt tgcagctgat gctctgctg 339

<210> 268  
 <211> 153  
 <212> DNA  
 <213> Mouse

<400> 268  
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 gcattccacc atgagctgaa gcaagccatt tgcagatgct ttactgggta tacgggacaa 120  
 cgatgtgagc atttgaccct aacttcgtat gct 153

<210> 269  
 <211> 153  
 <212> DNA  
 <213> Human

<400> 269  
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 gcattccacc atgagctaga gaaagccato tgcagggtgt ttactgggta tactggagaa 120  
 aggtgtgagc acttgacttt aacttcatat gct 153

<210> 270  
 <211> 288  
 <212> DNA  
 <213> Human

<400> 270  
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tgcaagtgtct	cccgaagg	acccaagatc	cgctacagcg	acgtgaagaa	gctggaaatg	120
aagcgaagt	acccgcactg	cgaggagaag	atgggttatca	tcaccaccaa	gagcgtgtcc	180
aggtaccgag	gtcaggagca	ctgcctgcac	cccaagctgc	agagcaccaa	gcgcttcac	240
aagtgtgtaca	acgcctggaa	cgagaagcgc	aggggtctacg	aagaatag		288

<210> 271  
 <211> 234  
 <212> DNA  
 <213> Mouse

<400> 271						
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gaaatgaagc	caaagtaccc	acactgcgag	gagaagatgg	ttatcgtcac	caccaagagc	120
atgtccaggt	accggggcca	ggagcactgc	ctgcacccta	agctgcagag	caccaaagcgc	180
ttcatcaagt	ggtacaatgc	ctggaacgag	aagcgcaggg	tctacgaaga	atag	234

<210> 272  
 <211> 234  
 <212> DNA  
 <213> Human

<400> 272						
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gaaatgaagc	caaagtaccc	gcactgcgag	gagaagatgg	ttatcatcac	caccaagagc	120
gtgtccaggt	accgaggtca	ggagcactgc	ctgcacccca	agctgcagag	caccaagcgc	180
ttcatcaagt	ggtacaacgc	ctggaacgag	aagcgcaggg	tctacgaaga	atag	234

<210> 273  
 <211> 645  
 <212> DNA  
 <213> Mouse

<400> 273						
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acctccgaca	tcttggaat	cagcactatg	gctaacgtct	ctgggtggga	tgtaacctat	180
acagtgcagg	tccccgtgaa	cgattcagtc	agtgcctgta	tcctgaaagc	agtgaaggag	240
gacgacagcc	cagtgggcac	ctggagtggg	acatatgaga	agtgcacga	cagcagtgtc	300
tactataact	tgacatocca	aagccagtcg	gtcttccaga	caaactggac	agttcctact	360
tccgaggatg	tgactaaagt	caacctgcag	gtcctcatcg	tcgtcaatcg	cacagcctca	420
aagtcattccg	tgaaaatgga	acaagtacaa	ccctcagcct	caacccctat	tcctgagagt	480
tctgagacca	gccagaccat	aaacacgact	ccaactgtga	acacagccaa	gactacagcc	540
aaggacacag	ccaacaccac	agccgtgacc	acagccaata	ccacagccaa	taccacagcc	600
gtgaccacag	ccaagaccac	agccaaaagc	ctggccatcc	gcact		645

<210> 274  
 <211> 63  
 <212> DNA  
 <213> Mouse

<400> 274						
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aac						63

<210> 275  
 <211> 388  
 <212> PRT  
 <213> Mouse

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      <400> 275
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Gly Ala Ala Gly Thr Asp Pro Pro Thr Ala Pro Thr Thr Ala Glu Arg
 20      25      30
Gln Arg Gln Pro Thr Asp Ile Ile Leu Asp Cys Phe Leu Val Thr Glu
 35      40      45
Asp Arg His Arg Gly Ala Phe Ala Ser Ser Gly Asp Arg Glu Arg Ala
 50      55      60
Leu Leu Val Leu Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu
 65      70      75      80
Gly Ile Thr Asp Phe Gln Gly Ser Thr Glu Thr Lys Gln Asp Ser Pro
 85      90      95
Val Ile Phe Glu Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu
 100      105      110
Ala Leu Leu His Ala Asp Cys Ser Gly Lys Ala Val Thr Cys Glu Ile
 115      120      125
Ser Lys Tyr Phe Leu Gln Ala Arg Gln Glu Ala Thr Phe Glu Lys Ala
 130      135      140
His Trp Phe Ile Ser Asn Met Gln Val Ser Arg Gly Gly Pro Ser Val
 145      150      155      160
Ser Met Val Met Lys Thr Leu Arg Asp Ala Glu Val Gly Ala Val Arg
 165      170      175
His Pro Thr Leu Asn Leu Pro Leu Ser Ala Gln Gly Thr Val Lys Thr
 180      185      190
Gln Val Glu Phe Gln Val Thr Ser Glu Thr Gln Thr Leu Asn His Leu
 195      200      205
Leu Gly Ser Ser Val Ser Leu His Cys Ser Phe Ser Met Ala Pro Asp
 210      215      220
Leu Asp Leu Thr Gly Val Glu Trp Arg Leu Gln His Lys Gly Ser Gly
 225      230      235      240
Gln Leu Val Tyr Ser Trp Lys Thr Gly Gln Gly Gln Ala Lys Arg Lys
 245      250      255
Gly Ala Thr Leu Glu Pro Glu Glu Leu Leu Arg Ala Gly Asn Ala Ser
 260      265      270
Leu Thr Leu Pro Asn Leu Thr Leu Lys Asp Glu Gly Thr Tyr Ile Cys
 275      280      285
Gln Ile Ser Thr Ser Leu Tyr Gln Ala Gln Gln Ile Met Pro Leu Asn
 290      295      300
Ile Leu Ala Pro Pro Lys Val Gln Leu His Leu Ala Asn Lys Asp Pro
 305      310      315      320
Leu Pro Ser Leu Val Cys Ser Ile Ala Gly Tyr Tyr Pro Leu Asp Val
 325      330      335
Gly Val Thr Trp Ile Arg Glu Glu Leu Gly Gly Ile Pro Ala Gln Val
 340      345      350
Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Thr Met Gly Thr Tyr
 355      360      365
Ser Ile Ser Ser Thr Val Met Ala Asp Pro Gly Pro Thr Gly Ala Thr
 370      375      380
Tyr Thr Cys Gln
385

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      <210> 276
      <211> 151
      <212> PRT
      <213> Rat

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<400> 276  
 Met Ala Glu Pro Trp Ala Gly Gln Phe Leu Gln Ala Leu Pro Ala Thr  
 1 5 10 15  
 Val Leu Gly Ala Leu Gly Thr Leu Gly Ser Glu Phe Leu Arg Glu Trp  
 20 25 30  
 Glu Thr Gln Asp Met Arg Val Thr Leu Phe Lys Leu Leu Leu Trp  
 35 40 45  
 Leu Val Leu Ser Leu Leu Gly Ile Gln Leu Ala Trp Gly Phe Tyr Gly  
 50 55 60  
 Asn Thr Val Thr Gly Leu Tyr His Arg Pro Gly Lys Trp Gln Gln Met  
 65 70 75 80  
 Lys Leu Ser Lys Leu Thr Glu Asn Lys Gly Arg Gln Gln Glu Lys Gly  
 85 90 95  
 Leu Gln Arg Tyr Arg Trp Val Cys Trp Leu Leu Cys Cys Thr Leu Leu  
 100 105 110  
 Leu Ser Arg Pro Leu Arg Gln Leu Gln Arg Ala Trp Val Gly Gly Leu  
 115 120 125  
 Glu Tyr His Asp Ala Pro Arg Val Ser Leu His Cys Pro Gln Pro Cys  
 130 135 140  
 Leu Gln Gln Arg Gln Val Leu  
 145 150

<210> 277  
 <211> 163  
 <212> PRT  
 <213> Rat

<400> 277  
 Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr  
 1 5 10 15  
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe  
 20 25 30  
 Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala  
 35 40 45  
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn  
 50 55 60  
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val  
 65 70 75 80  
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu  
 85 90 95  
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr  
 100 105 110  
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys  
 115 120 125  
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser  
 130 135 140  
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg  
 145 150 155 160  
 Trp Lys Asn

<210> 278  
 <211> 330  
 <212> PRT  
 <213> Rat

<400> 278

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Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1          5          10          15
Ala Leu Trp Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
 20          25          30
Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35          40          45
Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50          55          60
Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65          70          75          80
Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85          90          95
Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
 100          105          110
Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
 115          120          125
Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
 130          135          140
Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
 145          150          155          160
Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
 165          170          175
Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
 180          185          190
Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
 195          200          205
Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
 210          215          220
Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
 225          230          235          240
Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
 245          250          255
Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
 260          265          270
Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
 275          280          285
Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
 290          295          300
Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
 305          310          315          320
His Arg Lys Ala Phe Leu Pro Phe Leu Phe
 325          330

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&lt;210&gt; 279

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 279

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Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
 1          5          10          15
His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
 20          25          30
Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
 35          40          45
Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
 50          55          60

```

&lt;210&gt; 280

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 280

```

Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
 1          5          10          15
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
 20          25          30
Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
 35          40          45
Phe Arg Gly Tyr Gln Gly Pro Gly Pro Gly Pro Gly Ile
 50          55          60
Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
 65          70          75          80
Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
 85          90          95
Glu Arg Gly Gln His Gly Pro Lys Gly
 100          105

```

&lt;210&gt; 281

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 281

```

Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
 1          5          10          15
Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
 20          25

```

&lt;210&gt; 282

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 282

```

Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1          5          10          15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20          25          30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35          40          45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50          55          60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65          70          75          80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85          90          95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
 100          105          110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
 115          120          125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
 130          135          140

```

Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu  
 145 150 155 160  
 Gly Glu Met Pro Pro Glu Asp Gly Met  
 165

<210> 283  
 <211> 61  
 <212> PRT  
 <213> Mouse

<400> 283  
 Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile  
 1 5 10 15  
 Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val  
 20 25 30  
 Thr Val Thr Gln Met Arg Thr Ile Ile Thr Met Asp Gln Leu Arg  
 35 40 45  
 Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser  
 50 55 60

<210> 284  
 <211> 131  
 <212> PRT  
 <213> Mouse

<400> 284  
 Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala  
 1 5 10 15  
 Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg  
 20 25 30  
 Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln  
 35 40 45  
 Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala  
 50 55 60  
 Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr  
 65 70 75 80  
 Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg  
 85 90 95  
 Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu  
 100 105 110  
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser  
 115 120 125  
 Leu Arg Arg  
 130

<210> 285  
 <211> 78  
 <212> PRT  
 <213> Mouse

<400> 285  
 Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys  
 1 5 10 15  
 Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser  
 20 25 30  
 Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu  
 35 40 45

Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His  
 50 55 60  
 Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val  
 65 70 75

<210> 286  
 <211> 206  
 <212> PRT  
 <213> Mouse

<400> 286  
 Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile  
 1 5 10 15  
 Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu  
 20 25 30  
 Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser  
 35 40 45  
 Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly  
 50 55 60  
 Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser  
 65 70 75 80  
 Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys  
 85 90 95  
 Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn  
 100 105 110  
 Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser  
 115 120 125  
 Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln  
 130 135 140  
 Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val  
 145 150 155 160  
 Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser  
 165 170 175  
 His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg  
 180 185 190  
 Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser  
 195 200 205

<210> 287  
 <211> 169  
 <212> PRT  
 <213> Mouse

<400> 287  
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly  
 1 5 10 15  
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg  
 20 25 30  
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly  
 35 40 45  
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln  
 50 55 60  
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu  
 65 70 75 80  
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr  
 85 90 95  
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly

100 105 110  
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe  
 115 120 125  
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu  
 130 135 140  
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu  
 145 150 155 160  
 Gly Glu Met Pro Pro Glu Asp Gly Met  
 165

<210> 288  
 <211> 114  
 <212> PRT  
 <213> Mouse

<400> 288  
 Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu  
 1 5 10 15  
 Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp  
 20 25 30  
 Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu  
 35 40 45  
 Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile  
 50 55 60  
 His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys  
 65 70 75 80  
 Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys  
 85 90 95  
 Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val  
 100 105 110  
 Ser Leu

<210> 289  
 <211> 46  
 <212> PRT  
 <213> Mouse

<400> 289  
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys  
 1 5 10 15  
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu  
 20 25 30  
 Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn  
 35 40 45

<210> 290  
 <211> 199  
 <212> PRT  
 <213> Mouse

<400> 290  
 Met Val Leu Pro Thr Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly  
 1 5 10 15  
 Leu Gly Gly Glu Thr Arg Pro Arg Ala Ala Thr Glu Arg Arg Ser Val  
 20 25 30  
 Gly Pro Ser Ala Arg Arg Gly Ala Gly Pro Arg Val Ser Gly Leu Leu

```

      35      40      45
Gly Phe Cys Gln Leu Ser Gln Leu Ala Ser Ala Asp Pro Glu Arg Arg
 50      55      60
Ser Pro Arg Ala Ile Val Pro Arg Ala Pro Arg Pro Arg Ser Arg Arg
65      70      75      80
Arg Pro Cys Leu Pro Gly Phe Ser Arg Arg Phe Pro Arg Glu Arg Arg
      85      90      95
Ser Pro Gly Gln Pro Pro Ser Arg Thr Pro Gln Pro Pro Gln Pro Cys
      100      105      110
Arg Gly Pro Ser Pro Gly Thr Ala Gln Thr Arg Ser Asn Leu Arg Gly
      115      120      125
Trp Gln Arg Gly Gly Ser Ile Val Leu Gln Ala Ser Glu Arg Thr Arg
      130      135      140
Ala Gly Cys Arg Thr Pro Val Cys Val Ser His Pro Ser Ala Phe Pro
      145      150      155      160
Pro Pro Arg Ala Leu Phe Gly Val Phe Val Ala Ser Ala Pro Glu Val
      165      170      175
Val Cys Val Cys Val Ser Val Val Leu Ser Val Cys Leu Leu Ser Pro
      180      185      190
Arg Gly Lys Thr Leu Val Asp
      195

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<210> 291
<211> 568
<212> PRT
<213> Rat

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      <400> 291
Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1      5      10      15
Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
      20      25      30
Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
      35      40      45
Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
      50      55      60
Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
      65      70      75      80
Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
      85      90      95
Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
      100      105      110
Gln Lys Gln Gln Met Thr Asp Val Glu Gly Thr Glu Leu Phe Ser Tyr
      115      120      125
Lys Gly Asn Asp Val Glu Tyr Phe Leu Ser Ser Ser Pro Ser Gly
      130      135      140
Leu Tyr Gln Leu Glu Leu Leu Ser Thr Glu Lys Asp Thr His Phe Lys
      145      150      155      160
Val Tyr Ala Thr Thr Pro Glu Ser Asp Gln Pro Tyr Pro Asp Leu
      165      170      175
Pro Tyr Asp Pro Arg Val Asp Val Thr Ser Ile Gly Arg Thr Thr Val
      180      185      190
Thr Leu Ala Trp Lys Gln Ser Pro Thr Ala Ser Met Leu Lys Gln Pro
      195      200      205
Ile Glu Tyr Cys Val Val Ile Asn Lys Glu His Asn Phe Lys Ser Leu
      210      215      220
Cys Ala Ala Glu Thr Lys Met Ser Ala Asp Asp Ala Phe Met Val Ala

```

```
<210> 292
<211> 123
<212> PRT
<213> Mouse
```

118



50                      55                      60  
 Gly Gln Glu Phe Arg Phe Gly Ser Cys Gln Val Thr Gly Val Val Leu  
 65                      70                      75                      80  
 Pro Glu Leu Trp Glu Ala Phe Trp Thr Val Lys Asn Thr Val Gln Thr  
                     85                      90                      95  
 Gln Asp Asp Ile Thr Ser Ile Arg Leu Leu Lys Pro Gln Val Leu Arg  
                     100                      105                      110  
 Asn Val Ser Val Ile Arg Trp Glu Gly Asp Ser  
                     115                      120

<210> 293  
 <211> 66  
 <212> PRT  
 <213> Mouse

<400> 293  
 Met Asp Val Trp Ser Gly Leu Pro Leu Glu Thr Leu Trp Ile Tyr Glu  
 1                      5                      10                      15  
 Ala Val Leu Pro Trp Leu Leu Met Gly Gln Gly His Ala Trp Val Cys  
                     20                      25                      30  
 Gly Pro Ile Ala Leu Trp Val Phe Val Asn Val Pro Gly Leu Cys Tyr  
                     35                      40                      45  
 His Gln Lys Pro Phe Arg Cys Pro Trp Ser Gly Leu Leu Pro Glu Ala  
                     50                      55                      60  
 Leu Cys  
 65

<210> 294  
 <211> 294  
 <212> PRT  
 <213> Rat

<400> 294  
 Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu  
 1                      5                      10                      15  
 Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala  
                     20                      25                      30  
 Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro  
                     35                      40                      45  
 Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly  
                     50                      55                      60  
 Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln  
                     65                      70                      75                      80  
 Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr  
                     85                      90                      95  
 Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly  
                     100                      105                      110  
 Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys  
                     115                      120                      125  
 His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro  
                     130                      135                      140  
 Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala  
                     145                      150                      155                      160  
 Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile  
                     165                      170                      175  
 Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser  
                     180                      185                      190

Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Tyr Tyr Phe Thr Tyr  
 195 200 205  
 Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile Gly Leu Val His Asn  
 210 215 220  
 Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn His Asp  
 225 230 235 240  
 Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp Glu Val  
 245 250 255  
 Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro  
 260 265 270  
 Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln  
 275 280 285  
 Gly Asp Pro Asn Glu Val  
 290

&lt;210&gt; 295

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 295

Met Arg Pro Leu Leu Ala Leu Leu Leu Gly Leu Ala Ser Gly Ser  
 1 5 10 15  
 Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly Gln Pro  
 20 25 30  
 Gly Leu Pro Gly Thr Pro Gly His Gly Ser Gln Gly Leu Pro Gly  
 35 40 45  
 Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu  
 50 55 60  
 Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Glu Pro  
 65 70 75 80  
 Gly Pro Arg Gly Glu Ala Gly Pro Val Gly Ala Ile Gly Pro Ala Gly  
 85 90 95  
 Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu  
 100 105 110  
 Ser Arg Val Pro Pro Pro Ala Asp Thr Pro Leu Pro Phe Asp Arg Val  
 115 120 125  
 Leu Leu Asn Glu Gln Gly His Tyr Asp Ala Thr Thr Gly Lys Phe Thr  
 130 135 140  
 Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr  
 145 150 155 160  
 Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala  
 165 170 175  
 Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser  
 180 185 190  
 Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln  
 195 200 205  
 Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp  
 210 215 220  
 Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro  
 225 230 235 240  
 Val Phe Ala

&lt;210&gt; 296

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 296

Met	Leu	Val	Ala	Phe	Leu	Gly	Ala	Ser	Ala	Val	Thr	Ala	Ser	Thr	Gly
1				5					10					15	
Leu	Leu	Trp	Lys	Lys	Ala	His	Ala	Glu	Ser	Pro	Pro	Ser	Val	Asn	Ser
			20					25					30		
Lys	Lys	Thr	Asp	Ala	Gly	Asp	Lys	Gly	Lys	Ser	Lys	Asp	Thr	Arg	Glu
			35					40				45			
Val	Ser	Ser	His	Glu	Gly	Ser	Ala	Ala	Asp	Thr	Ala	Ala	Glu	Pro	Tyr
			50				55				60				
Pro	Glu	Glu	Lys	Lys	Lys	Arg	Ser	Gly	Phe	Arg	Asp	Arg	Lys	Val	
65					70				75					80	
Met	Glu	Tyr	Glu	Asn	Arg	Ile	Arg	Ala	Tyr	Ser	Thr	Pro	Asp	Lys	Ile
				85					90					95	
Phe	Arg	Tyr	Phe	Ala	Thr	Leu	Lys	Val	Ile	Asn	Glu	Pro	Gly	Glu	Thr
				100				105					110		
Glu	Val	Phe	Met	Thr	Pro	Gln	Asp	Phe	Val	Arg	Ser	Ile	Thr	Pro	Asn
				115			120					125			
Glu	Lys	Gln	Pro	Glu	His	Leu	Gly	Leu	Asp	Gln	Tyr	Ile	Ile	Lys	Arg
				130			135				140				
Phe	Asp	Gly	Lys	Lys	Ile	Ala	Gln	Glu	Arg	Glu	Lys	Phe	Ala	Asp	Glu
145					150					155					160
Gly	Ser	Ile	Phe	Tyr	Thr	Leu	Gly	Glu	Cys	Gly	Leu	Ile	Ser	Phe	Ser
				165					170					175	
Asp	Tyr	Ile	Phe	Leu	Thr	Thr	Val	Leu	Ser	Thr	Pro	Gln	Arg	Asn	Phe
				180				185					190		
Glu	Ile	Ala	Phe	Lys	Met	Phe	Asp	Leu	Asn	Gly	Asp	Gly	Glu	Val	Asp
				195			200					205			
Met	Glu	Glu	Phe	Glu	Gln	Val	Gln	Ser	Ile	Ile	Arg	Ser	Gln	Thr	Ser
				210			215				220				
Met	Gly	Met	Arg	His	Arg	Asp	Arg	Pro	Thr	Thr	Gly	Asn	Thr	Leu	Lys
225					230					235					240
Ser	Gly	Leu	Cys	Ser	Ala	Leu	Thr	Thr	Tyr	Phe	Phe	Gly	Ala	Asp	Leu
				245					250					255	
Lys	Gly	Lys	Leu	Thr	Ile	Lys	Asn	Phe	Leu	Glu	Phe	Gln	Arg	Lys	Leu
				260				265					270		
Gln	His	Asp	Val	Leu	Lys	Leu	Glu	Phe	Glu	Arg	His	Asp	Pro	Val	Asp
				275			280					285			
Gly	Arg	Ile	Ser	Glu	Arg	Gln	Phe	Gly	Gly	Met	Leu	Leu	Ala	Tyr	Ser
				290			295					300			
Gly	Val	Gln	Ser	Lys	Lys	Leu	Thr	Ala	Met	Gln	Arg	Gln	Leu	Lys	Lys
305					310					315					320
His	Phe	Lys	Asp	Gly	Lys	Gly	Leu	Thr	Phe	Gln	Glu	Val	Glu	Asn	Phe
				325					330					335	
Phe	Thr	Phe	Leu	Lys	Asn	Ile	Asn	Asp	Val	Asp	Thr	Ala	Leu	Ser	Phe
				340				345					350		
Tyr	His	Met	Ala	Gly	Ala	Ser	Leu	Asp	Lys	Val	Thr	Met	Gln	Gln	Val
				355				360					365		
Ala	Arg	Thr	Val	Ala	Lys	Val	Glu	Leu	Ser	Asp	His	Val	Cys	Asp	Val
				370			375				380				
Val	Phe	Ala	Leu	Phe	Asp	Cys	Asp	Gly	Asn	Gly	Glu	Leu	Ser	Asn	Lys
385					390					395					400
Glu	Phe	Val	Ser	Ile	Met	Lys	Gln	Arg	Leu	Met	Arg	Gly	Leu	Glu	Lys
				405					410					415	
Pro	Lys	Asp	Met	Gly	Phe	Thr	Arg	Leu	Met	Gln	Ala	Met	Trp	Lys	Cys
				420				425					430		

Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys  
 435 440

<210> 297  
 <211> 65  
 <212> PRT  
 <213> Human

<400> 297  
 Met Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser  
 1 5 10 15  
 Arg Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser  
 20 25 30  
 Trp Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala  
 35 40 45  
 Leu Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser  
 50 55 60  
 Leu  
 65

<210> 298  
 <211> 52  
 <212> PRT  
 <213> Human

<400> 298  
 Met Lys Ile Asn Ile Ile Gln Gly Ser Ile Met Ile Leu Leu Ile Cys  
 1 5 10 15  
 Leu Ser Gln Thr Cys Thr Ser Leu Pro Val Gln Glu Ala Leu Ile Thr  
 20 25 30  
 Phe Cys His Leu Tyr Phe Thr Tyr Cys Tyr Ser Gly Asn Ser Asn Lys  
 35 40 45  
 Met Gln Val Leu  
 50

<210> 299  
 <211> 41  
 <212> PRT  
 <213> Human

<400> 299  
 Met Pro Cys Val Leu Phe Phe Phe Phe Phe Leu Ser Thr Ser Lys Ser  
 1 5 10 15  
 Met Ile Tyr Ser Ser Leu Met Leu Gly Leu Tyr Ile Pro Ser Glu Ala  
 20 25 30  
 Cys Val Leu Gly Leu Lys Phe Lys Phe  
 35 40

<210> 300  
 <211> 80  
 <212> PRT  
 <213> Mouse

<400> 300  
 Met Val Trp Gly Thr Leu Leu Gly Arg Val Leu Ala Ala Leu Leu Asn  
 1 5 10 15  
 Ile Val Pro Thr Glu Ser Ser Tyr Arg Ser Pro Ser Phe Leu Ala Gly

```
<210> 301
<211> 82
<212> PRT
<213> Mouse
```

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<210> 302
<211> 411
<212> PRT
<213> Rat
```

123

Val Val Glu Val Trp Ser Gln Leu Leu Ser Gln Lys His Val Gly Leu  
 195 200 205  
 Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu  
 210 215 220  
 Leu Val Ile Leu Val Ile Pro Pro Ala Val Thr Pro Gly Thr Asp Gln  
 225 230 235 240  
 Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Ile Leu  
 245 250 255  
 Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ser Gln Gln Pro  
 260 265 270  
 Gly Pro Asn Ala Pro Leu Ser Trp Ile Arg Ala Cys Val Gln Val Leu  
 275 280 285  
 Asp Pro Lys Ser Gln Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe  
 290 295 300  
 Tyr Gly Met Asp Tyr Ala Ala Ser Lys Asp Ala Arg Glu Pro Val Ile  
 305 310 315 320  
 Gly Ala Arg Ala Val Leu Lys Val Ala Leu Pro Leu Ala Val Ser Ser  
 325 330 335  
 Gln Gln Ile Trp Thr Leu Gly Arg Gly Gly Ser Thr Ser Ala Leu Leu  
 340 345 350  
 Leu Ala Gly Leu Gly Leu Ala Ser Glu Pro Cys Thr Lys Ser Glu Glu  
 355 360 365  
 Val Pro Lys Lys Ser Leu Leu Asp Thr Val Trp His Trp Gln Gly Glu  
 370 375 380  
 Pro Gly Ala Leu Cys Arg Gly Arg Leu His Thr Trp Ile Leu Val Ser  
 385 390 395 400  
 Ala Val Pro Gln Ala Cys Thr Cys Leu Phe Gln  
 405 410

<210> 303  
 <211> 617  
 <212> PRT  
 <213> Mouse

<400> 303

Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu  
 1 5 10 15  
 Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg  
 20 25 30  
 Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe  
 35 40 45  
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys  
 50 55 60  
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser  
 65 70 75 80  
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His  
 85 90 95  
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr  
 100 105 110  
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu  
 115 120 125  
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu  
 130 135 140  
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala  
 145 150 155 160  
 Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser  
 165 170 175

```

Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
      180      185      190
Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
      195      200      205
Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp
      210      215      220
Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp
225      230      235      240
Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro
      245      250      255
Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro
      260      265      270
Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
      275      280      285
Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
      290      295      300
Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
305      310      315      320
Pro Ser Trp Thr Val Ser Met Asp Thr Gln Ala Gln Gln Leu Thr Leu
      325      330      335
His Phe Ser Ser Arg Thr Tyr Ala Thr Phe Ser Ala Ala Trp Ser Asp
      340      345      350
Pro Gly Leu Gly Pro Asp Thr Pro Met Pro Pro Val Tyr Ser Ile Ser
      355      360      365
Gln Thr Gln Gly Ser Val Pro Val Thr Leu Asp Leu Ile Ile Pro Phe
      370      375      380
Leu Arg Gln Glu Asn Cys Ile Leu Val Trp Arg Ser Asp Val His Phe
385      390      395      400
Ala Trp Lys His Val Leu Cys Pro Asp Asp Ala Pro Tyr Pro Thr Gln
      405      410      415
Leu Leu Leu Arg Ser Leu Gly Ser Gly Arg Thr Arg Pro Val Leu Leu
      420      425      430
Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly Ala Leu
      435      440      445
Ala Glu Leu Leu Arg Thr Ala Leu Gly Gly Gly Arg Asp Val Ile Val
      450      455      460
Asp Leu Trp Glu Gly Thr His Val Ala Arg Ile Gly Pro Leu Pro Trp
465      470      475      480
Leu Trp Ala Ala Arg Glu Arg Val Ala Arg Glu Gln Gly Thr Val Leu
      485      490      495
Leu Leu Trp Asn Cys Ala Gly Pro Ser Thr Ala Cys Ser Gly Asp Pro
      500      505      510
Gln Ala Ala Ser Leu Arg Thr Leu Leu Cys Ala Ala Pro Arg Pro Leu
      515      520      525
Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp Ile Pro Arg
      530      535      540
Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp Leu Pro Arg
545      550      555      560
Leu Leu Arg Ala Leu Asp Ala Gln Pro Ala Thr Leu Ala Ser Ser Trp
      565      570      575
Ser His Leu Gly Ala Lys Arg Cys Leu Lys Asn Arg Leu Glu Gln Cys
      580      585      590
His Leu Leu Glu Leu Glu Ala Ala Lys Asp Asp Tyr Gln Gly Ser Thr
      595      600      605
Asn Ser Pro Cys Gly Phe Ser Cys Leu
610      615

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<210> 304  
 <211> 72  
 <212> PRT  
 <213> Mouse

<400> 304  
 Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu  
 1 5 10 15  
 Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu  
 20 25 30  
 Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg  
 35 40 45  
 Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met  
 50 55 60  
 Ala Phe Ser Ile Leu Phe Ile Gln  
 65 70

<210> 305  
 <211> 649  
 <212> PRT  
 <213> Mouse

<400> 305  
 Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly  
 1 5 10 15  
 Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro  
 20 25 30  
 Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser  
 35 40 45  
 Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr  
 50 55 60  
 Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys  
 65 70 75 80  
 Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp  
 85 90 95  
 Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln  
 100 105 110  
 Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro  
 115 120 125  
 Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser  
 130 135 140  
 Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe  
 145 150 155 160  
 Leu Ser Arg Asn His Leu Ser Thr Ile Pro Gly Gly Leu Pro Arg Thr  
 165 170 175  
 Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser  
 180 185 190  
 Pro Ser Leu His Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly  
 195 200 205  
 Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu  
 210 215 220  
 Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala  
 225 230 235 240  
 Pro Val Asn Leu Pro Gly Thr Ser Leu Arg Lys Leu Tyr Leu Gln Asp  
 245 250 255  
 Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln  
 260 265 270



Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln  
 275 280 285  
 Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn  
 290 300  
 Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu  
 305 310 315 320  
 Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala  
 325 330 335  
 Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Ser Ala Glu Leu  
 340 345 350  
 Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr  
 355 360 365  
 Ala Ile Pro Asn Thr Ala Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro  
 370 375 380  
 Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Ile Lys Asp Gln  
 385 390 395 400  
 Arg Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Leu Ile Thr Val Lys  
 405 410 415  
 Ser Val Thr Pro Asp Thr Ile His Ile Ser Trp Arg Leu Ala Leu Pro  
 420 425 430  
 Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala  
 435 440 445  
 Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr  
 450 455 460  
 Leu Val Thr Ala Leu Glu Pro Glu Ser Pro Tyr Arg Val Cys Met Val  
 465 470 475 480  
 Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys  
 485 490 495  
 Ile Glu Thr Gln Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr  
 500 505 510  
 Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro  
 515 520 525  
 Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Ser Ile Ala Leu  
 530 535 540  
 Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser  
 545 550 555 560  
 Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala  
 565 570 575  
 Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr  
 580 585 590  
 Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu  
 595 600 605  
 Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys  
 610 615 620  
 Asn Asn Leu Ser Glu Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly  
 625 630 635 640  
 Ile Pro Asp Ser Asp His Ser His Ser  
 645

<210> 306  
 <211> 150  
 <212> PRT  
 <213> Rat

<400> 306

Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala  
 1 5 10 15

Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser  
                   20                  25                  30  
 Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln  
                   35                  40                  45  
 Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala  
                   50                  55                  60  
 Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val  
 65                  70                  75                  80  
 Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr  
                   85                  90                  95  
 Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys Trp Ile Pro Arg Ala Ala  
                   100                  105                  110  
 Gly Leu Cys Ser Trp Cys Gly Gly Gly Leu Cys Val Arg Gly Ala His  
                   115                  120                  125  
 Leu His Ala Leu Asp Glu His Gly Gly Gln Leu Leu Arg Pro Leu Arg  
 130                  135                  140  
 Val Arg Ser Arg Leu Leu  
 145                  150

&lt;210&gt; 307

&lt;211&gt; 580

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 307

Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu  
   1                  5                  10                  15  
 Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu  
                   20                  25                  30  
 Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala  
                   35                  40                  45  
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly  
                   50                  55                  60  
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser  
 65                  70                  75                  80  
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp  
                   85                  90                  95  
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala  
                   100                  105                  110  
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser  
                   115                  120                  125  
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu  
                   130                  135                  140  
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys  
 145                  150                  155                  160  
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala  
                   165                  170                  175  
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys  
                   180                  185                  190  
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys  
                   195                  200                  205  
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile  
                   210                  215                  220  
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu  
 225                  230                  235                  240  
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly  
                   245                  250                  255

Lys Lys Asp Trp Ser Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu  
 260 265 270  
 Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp Ile Thr Gly  
 275 280 285  
 Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser Pro Pro Pro Thr Ser  
 290 295 300  
 Thr Tyr Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Val Tyr  
 305 310 315 320  
 Asp Leu Phe Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile  
 325 330 335  
 Gln Leu Lys Trp Lys Arg Pro Pro Asp Asn Glu Ala Leu Pro Val Pro  
 340 345 350  
 Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln Lys Gly  
 355 360 365  
 Glu Leu Ser Thr Leu Leu Tyr Asn Ser His Pro Tyr Arg Ala Phe Pro  
 370 375 380  
 Val Leu Leu Leu Asp Ala Val Pro Trp Tyr Leu Arg Leu Tyr Val His  
 385 390 395 400  
 Thr Leu Thr Ile Thr Ser Lys Gly Lys Asp Asn Lys Pro Ser Tyr Ile  
 405 410 415  
 His Tyr Gln Pro Ala Gln Asp Arg Gln Gln Pro His Leu Leu Glu Met  
 420 425 430  
 Leu Ile Gln Leu Pro Ala Asn Ser Val Thr Lys Val Ser Ile Gln Phe  
 435 440 445  
 Glu Arg Ala Leu Leu Lys Trp Thr Glu Tyr Thr Pro Asp Pro Asn His  
 450 455 460  
 Gly Phe Tyr Val Ser Pro Ser Val Leu Ser Ala Leu Val Pro Ser Met  
 465 470 475 480  
 Val Ala Ala Lys Pro Val Asp Trp Glu Glu Ser Pro Leu Phe Asn Thr  
 485 490 495  
 Leu Phe Pro Val Ser Asp Gly Ser Ser Tyr Phe Val Arg Leu Tyr Thr  
 500 505 510  
 Glu Pro Leu Leu Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr  
 515 520 525  
 Asn Val Ile Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser  
 530 535 540  
 Phe Tyr Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Lys Ser  
 545 550 555 560  
 Gly Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly  
 565 570 575  
 Val Pro Pro Leu  
 580

&lt;210&gt; 308

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 308

Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys  
 1 5 10 15  
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser  
 20 25 30  
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile  
 35 40 45  
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu  
 50 55 60

Tyr His Ser Phe Val Ser Ser Val Phe Ser Leu Phe Met Ser Arg Thr  
 65 70 75 80  
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro  
 85 90 95  
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His  
 100 105 110  
 Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met  
 115 120 125  
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met  
 130 135 140  
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu  
 145 150 155 160  
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu  
 165 170 175  
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Ser  
 180 185 190  
 Val Leu Glu Pro Thr Gln Gly Arg Val Ile Leu Ala Leu Val Leu Pro  
 195 200 205  
 Phe His Pro Tyr Val Glu Asn Val Gly Gly Lys Trp Glu Lys Pro Ser  
 210 215 220  
 Glu Ile Leu Glu Ile Lys Gly Gln Asn Trp Glu Glu Gln Val Asn Ser  
 225 230 235 240  
 Leu Pro Glu Val Phe Arg Lys Ala Gly Phe Val Ile Glu Ala Phe Thr  
 245 250 255  
 Arg Leu Pro Tyr Leu Cys Glu Gly Asp Met Tyr Asn Asp Tyr Tyr Val  
 260 265 270  
 Leu Asp Asp Ala Val Phe Val Leu Arg Pro Val  
 275 280

<210> 309  
 <211> 37  
 <212> PRT  
 <213> Rat

<400> 309  
 Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile  
 1 5 10 15  
 Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys  
 20 25 30  
 Arg Ala Asp Val Leu  
 35

<210> 310  
 <211> 70  
 <212> PRT  
 <213> Mouse

<400> 310  
 Met Ala Ala Ser Trp Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala  
 1 5 10 15  
 Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ser Gly Leu  
 20 25 30  
 Glu Gln Val Arg Glu Arg Thr Trp Ala Trp Gln Leu Leu Gln Glu Ile  
 35 40 45  
 Lys Ala Leu Phe Gly Asn Thr Glu Val Arg Leu Ala Leu Thr Asp Glu  
 50 55 60  
 Pro Leu Lys Ile Ser Pro

65

70

<210> 311  
 <211> 58  
 <212> PRT  
 <213> Human

<400> 311  
 Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala  
 1 5 10 15  
 Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr  
 20 25 30  
 Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val  
 35 40 45  
 Gln Glu Pro Gln Gly Lys Ala Lys Arg His  
 50 55

<210> 312  
 <211> 52  
 <212> PRT  
 <213> Human

<400> 312  
 Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys  
 1 5 10 15  
 Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser  
 20 25 30  
 Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu  
 35 40 45  
 Glu Lys Thr Lys  
 50

<210> 313  
 <211> 70  
 <212> PRT  
 <213> Human

<400> 313  
 Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys  
 1 5 10 15  
 Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe  
 20 25 30  
 Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe  
 35 40 45  
 Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln  
 50 55 60  
 Pro Met Thr Pro Pro Trp  
 65 70

<210> 314  
 <211> 58  
 <212> PRT  
 <213> Mouse

<400> 314  
 Met Phe Ile Thr Pro Phe Lys Ala Phe Leu Pro Leu Tyr Leu Leu Thr  
 1 5 10 15

Glu Leu Ser Leu Ile Asp Ile Thr Ser Cys Asp Asp Leu Pro His Ser  
 20 25 30  
 Val Leu Pro Gln His Leu Ser Phe Glu Phe Val Leu Trp Ser Met Tyr  
 35 40 45  
 Leu Leu Ile Cys Cys Phe Val Ile Ile Phe  
 50 55

<210> 315  
 <211> 229  
 <212> PRT  
 <213> Rat

<400> 315  
 Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys  
 1 5 10 15  
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr  
 20 25 30  
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln  
 35 40 45  
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val  
 50 55 60  
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly  
 65 70 75 80  
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly  
 85 90 95  
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg  
 100 105 110  
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met  
 115 120 125  
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys  
 130 135 140  
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu  
 145 150 155 160  
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu  
 165 170 175  
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu  
 180 185 190  
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Met Lys  
 195 200 205  
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg  
 210 215 220  
 Glu Asp Thr Glu Phe  
 225

<210> 316  
 <211> 128  
 <212> PRT  
 <213> Rat

<400> 316  
 Arg Ala Glu Phe Gly Thr Ser Gly Glu Met Gly Asn Ala Ala Leu Gly  
 1 5 10 15  
 Ala Glu Leu Gly Val Arg Val Leu Leu Phe Val Ala Phe Leu Ala Thr  
 20 25 30  
 Glu Leu Leu Pro Pro Phe Gln Arg Arg Ile Gln Pro Glu Glu Leu Trp  
 35 40 45  
 Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Gly Pro

50                      55                      60  
 Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile Phe Phe Ala  
 65                      70                      75                      80  
 Lys Phe Leu Arg Lys Ala Asp Ala Thr Asp Ser Lys Gln Ala Cys Leu  
                     85                      90                      95  
 Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Ile Ile  
                     100                      105                      110  
 Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe  
                     115                      120                      125

<210> 317  
 <211> 75  
 <212> PRT  
 <213> Rat

<400> 317  
 Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile  
   1                      5                      10                      15  
 Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp  
                     20                      25                      30  
 Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val  
                     35                      40                      45  
 Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr  
   50                      55                      60  
 Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu  
   65                      70                      75

<210> 318  
 <211> 43  
 <212> PRT  
 <213> Human

<400> 318  
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys  
   1                      5                      10                      15  
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu  
                     20                      25                      30  
 Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn  
                     35                      40

<210> 319  
 <211> 86  
 <212> PRT  
 <213> Mouse

<400> 319  
 Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile  
   1                      5                      10                      15  
 Cys Val Phe Trp Asp Phe Ile Phe Ile Phe Phe Asn Val Leu Ser  
                     20                      25                      30  
 Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala  
                     35                      40                      45  
 Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly  
   50                      55                      60  
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp  
   65                      70                      75                      80  
 Leu Leu Ser Phe Pro Pro

85

<210> 320  
 <211> 60  
 <212> PRT  
 <213> Mouse

<400> 320

Lys	Gly	Pro	Glu	Val	Ser	Cys	Cys	Ile	Lys	Tyr	Phe	Ile	Phe	Gly	Phe
1				5					10					15	
Asn	Val	Ile	Phe	Trp	Phe	Leu	Gly	Ile	Thr	Phe	Leu	Gly	Ile	Gly	Leu
			20					25					30		
Trp	Ala	Trp	Asn	Glu	Lys	Gly	Val	Leu	Ser	Asn	Ile	Ser	Ser	Ile	Thr
		35					40						45		
Asp	Leu	Gly	Gly	Phe	Asp	Pro	Val	Trp	Leu	Phe	Leu				
	50					55					60				

<210> 321  
 <211> 160  
 <212> PRT  
 <213> Mouse

<400> 321

Ile	Arg	His	Glu	Ala	Glu	Ala	Gly	Arg	His	Gln	Pro	Glu	Gln	Leu	Ala
1				5					10					15	
Ala	Asp	Ser	Arg	Thr	Glu	Thr	Val	Gly	Pro	Arg	Gln	Ser	Asn	Gly	Leu
			20					25					30		
Thr	Gly	Pro	Gly	Leu	Pro	Thr	Trp	Gln	Leu	His	Pro	Val	Leu	Phe	Pro
		35					40					45			
Glu	Leu	Val	Leu	Trp	Val	Asn	Met	Val	Pro	Cys	Phe	Leu	Leu	Ser	Leu
	50					55					60				
Leu	Leu	Leu	Val	Arg	Pro	Ala	Pro	Val	Val	Ala	Tyr	Ser	Val	Ser	Leu
65					70					75				80	
Pro	Ala	Ser	Phe	Leu	Glu	Glu	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly
			85						90					95	
Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Leu	Pro	Pro	Arg	Thr	Pro	Ala	Phe
			100						105				110		
Ser	Pro	Thr	Pro	Gly	Arg	Thr	Gln	Pro	Thr	Ala	Pro	Val	Gly	Pro	Val
		115					120					125			
Pro	Pro	Thr	Asn	Leu	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr
	130					135					140				
Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Thr	Phe	Leu	Ile	Ser	Ser
145					150					155					160

<210> 322  
 <211> 54  
 <212> PRT  
 <213> Mouse

<400> 322

Arg	Leu	Gln	Val	Asp	Thr	Ser	Gly	Ser	Lys	Val	Leu	Phe	Leu	Phe	Phe
1				5					10					15	
Phe	Phe	Phe	Leu	Cys	Val	Cys	Val	Leu	Val	Cys	Cys	Cys	Phe	Gly	Phe
			20					25					30		
Pro	Gly	Thr	His	Ser	Val	Asp	Gln	Ala	Ser	Pro	Lys	Leu	Arg	Asn	Leu
		35					40					45			
Pro	Pro	Glu	Cys	Trp	Asp										



50

<210> 323  
 <211> 280  
 <212> PRT  
 <213> Mouse

&lt;400&gt; 323

Leu	Asp	Ser	Arg	Ala	Cys	Arg	Ser	Thr	Leu	Val	Asp	Pro	Lys	Asn	Ser
1				5					10					15	
Ala	Arg	Glu	Asn	Ile	Arg	Glu	Tyr	Val	Arg	Trp	Met	Met	Tyr	Trp	Ile
			20					25					30		
Val	Phe	Ala	Ile	Phe	Met	Ala	Ala	Glu	Thr	Phe	Thr	Asp	Ile	Phe	Ile
		35					40					45			
Ser	Trp	Ser	Gly	Pro	Arg	Ile	Gly	Arg	Pro	Trp	Gly	Trp	Glu	Gly	Pro
50						55					60				
His	His	His	His	His	Leu	Ala	Ser	Gly	Ser	His	Lys	Pro	Leu	Pro	Leu
65					70					75				80	
Leu	Thr	His	Arg	Phe	Pro	Phe	Tyr	Tyr	Glu	Phe	Lys	Met	Ala	Phe	Val
				85					90					95	
Leu	Trp	Leu	Leu	Ser	Pro	Tyr	Thr	Lys	Gly	Ala	Ser	Leu	Leu	Tyr	Arg
			100					105					110		
Lys	Phe	Val	His	Pro	Ser	Leu	Ser	Arg	His	Glu	Lys	Glu	Ile	Asp	Ala
			115					120				125			
Cys	Ile	Val	Gln	Ala	Lys	Glu	Arg	Ser	Tyr	Glu	Thr	Met	Leu	Ser	Phe
		130				135					140				
Gly	Lys	Arg	Ser	Leu	Asn	Ile	Ala	Ala	Ser	Ala	Ala	Val	Gln	Ala	Ala
145					150					155				160	
Thr	Lys	Ser	Gln	Gly	Ala	Leu	Ala	Gly	Arg	Leu	Arg	Ser	Phe	Ser	Met
			165					170					175		
Gln	Asp	Leu	Arg	Ser	Ile	Pro	Asp	Thr	Pro	Val	Pro	Thr	Tyr	Gln	Asp
			180					185					190		
Pro	Leu	Tyr	Leu	Glu	Asp	Gln	Val	Pro	Arg	Arg	Arg	Pro	Pro	Ile	Gly
		195					200					205			
Tyr	Arg	Pro	Gly	Gly	Leu	Gln	Gly	Ser	Asp	Thr	Glu	Asp	Glu	Cys	Trp
		210				215					220				
Ser	Asp	Asn	Glu	Ile	Val	Pro	Gln	Pro	Pro	Val	Gly	Pro	Arg	Glu	Lys
225					230					235				240	
Pro	Leu	Gly	Arg	Ser	Gln	Ser	Leu	Arg	Val	Val	Lys	Arg	Lys	Pro	Leu
			245					250					255		
Thr	Arg	Glu	Gly	Thr	Ser	Arg	Ser	Leu	Lys	Val	Arg	Thr	Pro	Lys	Lys
			260					265					270		
Ala	Met	Pro	Ser	Asp	Met	Asp	Ser								
		275					280								

<210> 324  
 <211> 166  
 <212> PRT  
 <213> Rat

&lt;400&gt; 324

Ala	Leu	Arg	Arg	Val	Gly	Met	Glu	Leu	Pro	Ala	Val	Asn	Leu	Lys	Val
1				5					10					15	
Ile	Leu	Leu	Val	His	Trp	Leu	Leu	Thr	Thr	Trp	Gly	Cys	Leu	Ala	Phe
			20					25					30		
Ser	Gly	Ser	Tyr	Ala	Trp	Gly	Asn	Phe	Thr	Ile	Leu	Ala	Leu	Gly	Val
		35					40					45			

Trp Ala Val Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu  
 50 55 60  
 Gly Gly Leu Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile  
 65 70 75 80  
 Phe Tyr Ser Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly  
 85 90 95  
 Met Ala Ile Phe Ser Leu Leu Leu Lys Pro Phe Ser Cys Cys Leu Val  
 100 105 110  
 Tyr His Met His Arg Glu Arg Gly Gly Glu Leu Pro Leu Arg Ser Asp  
 115 120 125  
 Phe Phe Gly Pro Ser Gln Glu His Ser Ala Tyr Gln Thr Ile Asp Ser  
 130 135 140  
 Ser Asp Ser Pro Ala Asp Pro Leu Ala Ser Leu Glu Asn Lys Gly Gln  
 145 150 155 160  
 Ala Ala Pro Arg Gly Tyr  
 165

&lt;210&gt; 325

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 325

Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala  
 1 5 10 15  
 Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu  
 20 25 30  
 Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro  
 35 40 45  
 Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu  
 50 55 60  
 Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu  
 65 70 75 80  
 Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly  
 85 90 95  
 Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe  
 100 105 110  
 Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val  
 115 120 125  
 Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr  
 130 135 140  
 Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Met Phe  
 145 150 155 160  
 Ile Val Cys Ala Ala Leu Ile Thr Arg Gln Lys His Lys Ala Thr Ala  
 165 170 175  
 Tyr Tyr Pro Ser Ser Phe Pro Glu Lys Lys Tyr Val Asp Gln Arg Asp  
 180 185 190  
 Arg Ala Gly Gly Pro His Ala Phe Ser Glu Val Pro Asp Arg Ala Pro  
 195 200 205  
 Asp Ser Arg Gln Glu Glu Gly Leu Asp Ser Ser Gln Gln Leu Gln Ala  
 210 215 220  
 Asp Ile Leu Ala Ala Thr Gln Asn Leu Arg Ser Pro Ala Arg Ala Leu  
 225 230 235 240  
 Pro Gly Ser Gly Glu Gly Thr Lys Gln Val Lys Gly Gly Ser Glu Glu  
 245 250 255  
 Glu Glu Glu Lys Glu Glu Glu Val Phe Ser Gly Gln Glu Glu Pro Arg  
 260 265 270

Glu Ala Pro Val Cys Gly Val Thr Glu Glu Lys Pro Glu Val Pro Asp  
 275 280 285  
 Glu Thr Ala Ser Ala Glu Ala Glu Gly Val Pro Ala Ala Ser Glu Gly  
 290 295 300  
 Gln Gly Glu Pro Glu Gly Ser Phe Ser Leu Ala Gln Glu Pro Gln Gly  
 305 310 315 320  
 Ala Ala Gly Pro Ser Glu Arg Ser Cys Ala Cys Asn Arg Ile Ser Pro  
 325 330 335  
 Asn Val

<210> 326  
 <211> 347  
 <212> PRT  
 <213> Human

<400> 326  
 Ala Trp Ser Arg Pro Arg Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala  
 1 5 10 15  
 Trp Gly Ile Val Leu Glu Thr Val Ala Thr Ala Gly Val Val Thr Ser  
 20 25 30  
 Val Ala Phe Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp  
 35 40 45  
 Ser Asn Arg Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly  
 50 55 60  
 Val Leu Gly Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp  
 65 70 75 80  
 Gly Ser Thr Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser  
 85 90 95  
 Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu  
 100 105 110  
 Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala  
 115 120 125  
 Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val  
 130 135 140  
 Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser Ala  
 145 150 155 160  
 Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Thr Tyr Val Leu Phe  
 165 170 175  
 Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser  
 180 185 190  
 Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu  
 195 200 205  
 Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro  
 210 215 220  
 Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala  
 225 230 235 240  
 Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp  
 245 250 255  
 Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala  
 260 265 270  
 Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg  
 275 280 285  
 Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp  
 290 295 300  
 Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro  
 305 310 315 320



Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys  
 35 40 45  
 Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg  
 50 55 60  
 Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp  
 65 70 75 80  
 Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro Arg  
 85 90 95  
 Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val  
 100 105

<210> 330  
 <211> 155  
 <212> PRT  
 <213> Human

<400> 330  
 Ser Val Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu  
 1 5 10 15  
 Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu  
 20 25 30  
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys  
 35 40 45  
 Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu  
 50 55 60  
 Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys  
 65 70 75 80  
 Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly  
 85 90 95  
 Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro  
 100 105 110  
 Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val  
 115 120 125  
 Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe  
 130 135 140  
 Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu  
 145 150 155

<210> 331  
 <211> 299  
 <212> PRT  
 <213> Human

<400> 331  
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30  
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45  
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60  
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95  
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser

```

      100      105      110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
      115      120      125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
      130      135      140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
145      150      155
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
      165      170      175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
      180      185      190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
      195      200      205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
      210      215      220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225      230      235
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
      245      250      255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
      260      265      270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
      275      280      285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
      290      295

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<210> 332
<211> 299
<212> PRT
<213> Mouse

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      <400> 332
Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
1      5      10      15
Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
      20      25      30
Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr
      35      40      45
Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
      50      55      60
Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg
65      70      75      80
Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
      85      90      95
Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
      100      105      110
Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
      115      120      125
Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
      130      135      140
Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
145      150      155      160
Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
      165      170      175
Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
      180      185      190
Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys

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      195      200      205
Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
  210      215      220
Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
  225      230      235
Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
      245      250      255
Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
      260      265      270
Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
      275      280      285
Pro Gln His Ser Ser Ser Lys Ala Met Lys His
  290      295

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<210> 333  
 <211> 109  
 <212> PRT  
 <213> Mouse

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      <400> 333
Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
  1      5      10
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
      20      25      30
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
      35      40      45
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
      50      55      60
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
      65      70      75      80
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr
      85      90      95
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
      100      105

```

<210> 334  
 <211> 787  
 <212> PRT  
 <213> Mouse

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      <400> 334
Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
  1      5      10      15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
      20      25
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
      35      40      45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
      50      55      60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
      65      70      75      80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
      85      90      95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
      100      105      110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
      115      120      125

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Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp  
 130 135 140  
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile  
 145 150 155 160  
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp  
 165 170 175  
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu  
 180 185 190  
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr  
 195 200 205  
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe  
 210 215 220  
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly  
 225 230 235 240  
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys  
 245 250 255  
 Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro Gln  
 260 265 270  
 Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys  
 275 280 285  
 Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu  
 290 295 300  
 Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg  
 305 310 315 320  
 Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser  
 325 330 335  
 Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly  
 340 345 350  
 Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro Ser Ser  
 355 360 365  
 Ser Ser Gly Lys Arg Leu Ser Ser Gly Val Ser Ser Val Asp Ser Ala Phe  
 370 375 380  
 Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr  
 385 390 395 400  
 Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala  
 405 410 415  
 Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln  
 420 425 430  
 Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala  
 435 440 445  
 Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn  
 450 455 460  
 Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met  
 465 470 475 480  
 Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg  
 485 490 495  
 Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His  
 500 505 510  
 Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Glu  
 515 520 525  
 Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met  
 530 535 540  
 His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu  
 545 550 555 560  
 Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro  
 565 570 575  
 Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Leu



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      580      585      590
Ala Lys Gln Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg
      595      600      605
Thr Pro Leu His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg
      610      615      620
Ile Leu Ile Asp Leu Cys Ser Asp Val Asn Ile Cys Ser Leu Gln Ala
      625      630      635
Gln Thr Pro Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala
      645      650      655
Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu Ala Leu Thr Ser Glu
      660      665      670
Gly Tyr Thr Ala Leu His Leu Ala Ala Gln Asn Gly His Leu Ala Thr
      675      680      685
Val Lys Leu Leu Ile Glu Glu Lys Ala Asp Val Met Ala Arg Gly Pro
      690      695      700
Leu Asn Gln Thr Ala Leu His Leu Ala Ala Ala Arg Gly His Ser Glu
      705      710      715
Val Val Glu Glu Leu Val Ser Ala Asp Leu Ile Asp Leu Ser Asp Glu
      725      730      735
Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ser Gln
      740      745      750
Thr Val Glu Thr Leu Leu Lys His Gly Ala His Ile Asn Leu Gln Ser
      755      760      765
Leu Lys Phe Gln Gly Gly Gln Ser Ser Ala Ala Thr Leu Leu Arg Arg
      770      775      780
Ser Lys Thr
      785

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<210> 335
<211> 194
<212> PRT
<213> Mouse

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      <400> 335
Pro Gly Cys Lys Ser Cys Thr Val Cys Arg His Gly Leu Cys Arg Ser
      5      10      15
Val Glu Lys Asp Ser Val Val Cys Glu Cys His Pro Gly Trp Thr Gly
      20      25      30
Pro Leu Cys Asp Gln Glu Ala Arg Asp Pro Cys Leu Gly His Ser Cys
      35      40      45
Arg His Gly Thr Cys Met Ala Thr Gly Asp Ser Tyr Val Cys Lys Cys
      50      55      60
Ala Glu Gly Tyr Gly Gly Ala Leu Cys Asp Gln Lys Asn Asp Ser Ala
      65      70      75
Ser Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
      85      90      95
Asp Arg Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly His
      100      105      110
His Cys Glu Gln Glu Asn Pro Cys Met Gly Glu Ile Val Arg Glu Ala
      115      120      125
Ile Arg Arg Gln Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val
      130      135      140
Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro
      145      150      155
Ile Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly Ser
      165      170      175
Ser Phe Val Glu Glu Val Glu Arg His Leu Glu Cys Gly Cys Arg Ala

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Cys Ser 180 185 190  
 <210> 336  
 <211> 274  
 <212> PRT  
 <213> Human  
 <400> 336  
 Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu Pro Gly Ser Phe Arg  
 1 5 10 15  
 Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro Asn Asn Arg Ser Cys  
 20 25 30  
 Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro Cys Glu Gln Arg Cys  
 35 40 45  
 Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys His Gln Gly Tyr Glu  
 50 55 60  
 Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile Asp Glu Cys Ser Tyr  
 65 70 75 80  
 Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn Glu Pro Gly Arg Phe  
 85 90 95  
 Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu Ala Thr Arg Leu Cys  
 100 105 110  
 Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His Gln Cys Ser Glu Ala  
 115 120 125  
 Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg Cys Val Asp Thr Asn  
 130 135 140  
 Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu Asn Arg Cys Leu Cys  
 145 150 155 160  
 Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro Ser Ser Ile Val His  
 165 170 175  
 Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val Pro Ala Asp Val Phe  
 180 185 190  
 Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala Tyr Asn Ala Phe Gln  
 195 200 205  
 Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr Ile Arg Gln Ile Asn  
 210 215 220  
 Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro Val Thr Gly Pro Arg  
 225 230 235 240  
 Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met Asn Ser Leu Met Ser  
 245 250 255  
 Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val Phe Val Gly Ala Tyr  
 260 265 270  
 Thr Phe

<210> 337  
 <211> 316  
 <212> PRT  
 <213> Mouse

<400> 337  
 His Glu Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn  
 1 5 10 15  
 Ile Asp Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr His  
 20 25 30

Val Met Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln  
 35 40 45  
 Ala Ile Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala  
 50 55 60  
 Lys Thr Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala  
 65 70 75 80  
 Ser Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys  
 85 90 95  
 Thr His Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg  
 100 105 110  
 Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys  
 115 120 125  
 Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala  
 130 135 140  
 Met Ser Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser  
 145 150 155 160  
 Thr Thr Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln  
 165 170 175  
 Leu Glu Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met  
 180 185 190  
 Arg Gly Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp  
 195 200 205  
 Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile  
 210 215 220  
 Ser Gly Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys  
 225 230 235 240  
 Arg Arg Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro  
 245 250 255  
 Ser Ala Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp  
 260 265 270  
 Leu Gly Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp  
 275 280 285  
 Glu Gln Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile  
 290 295 300  
 Leu Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys  
 305 310 315

<210> 338  
 <211> 237  
 <212> PRT  
 <213> Mouse

<400> 338  
 Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys  
 1 5 10 15  
 Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser  
 20 25 30  
 Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser  
 35 40 45  
 Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val  
 50 55 60  
 Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu  
 65 70 75 80  
 Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn  
 85 90 95  
 Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe  
 100 105 110

Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn  
 115 120 125  
 Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val  
 130 135 140  
 Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser  
 145 150 155 160  
 Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala  
 165 170 175  
 Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala  
 180 185 190  
 Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala  
 195 200 205  
 Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu  
 210 215 220  
 His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe  
 225 230 235

<210> 339  
 <211> 469  
 <212> PRT  
 <213> Mouse

<400> 339  
 Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr  
 1 5 10 15  
 Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser  
 20 25 30  
 Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr  
 35 40 45  
 Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp  
 50 55 60  
 Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu  
 65 70 75 80  
 Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly  
 85 90 95  
 Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val  
 100 105 110  
 Lys Ile Ser Glu Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys  
 115 120 125  
 Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu  
 130 135 140  
 Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His  
 145 150 155 160  
 Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe  
 165 170 175  
 Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala  
 180 185 190  
 Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp  
 195 200 205  
 Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met  
 210 215 220  
 Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys  
 225 230 235 240  
 Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu  
 245 250 255  
 Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly  
 260 265 270

Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser  
 275 280 285  
 Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu  
 290 295 300  
 Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu  
 305 310 315 320  
 Asp Cys Ala Arg Arg Ile Leu Ala Lys Glu Gly Val Ala Ala Phe Tyr  
 325 330 335  
 Lys Gly Tyr Ile Pro Asn Met Leu Gly Ile Ile Pro Tyr Ala Gly Ile  
 340 345 350  
 Asp Leu Ala Val Tyr Glu Thr Leu Lys Asn Thr Trp Leu Gln Arg Tyr  
 355 360 365  
 Ala Val Asn Ser Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly  
 370 375 380  
 Thr Ile Ser Ser Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu  
 385 390 395 400  
 Val Arg Thr Arg Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu  
 405 410 415  
 Val Thr Met Ser Ser Leu Phe Lys Gln Ile Leu Arg Thr Glu Gly Ala  
 420 425 430  
 Phe Gly Leu Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro  
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 Ala Val Ser Ile Ser Tyr Val Tyr Glu Asn Leu Lys Ile Thr Leu  
 450 455 460  
 Gly Val Gln Ser Arg  
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<210> 340  
 <211> 99  
 <212> PRT  
 <213> Mouse

<400> 340  
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 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro  
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 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 35 40 45  
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser  
 50 55 60  
 Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr  
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 Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val  
 85 90 95  
 Tyr Glu Glu

<210> 341  
 <211> 431  
 <212> PRT  
 <213> Mouse

<400> 341  
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 Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr

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Gln	Leu	Trp	Leu	Phe	Arg	Phe	Leu	Leu	Asn	Val	Ala	Gly	Tyr	Ala	Ser
		35					40					45			
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	50					55					60				
Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys
65				70					75						80
Val	Phe	Gly	Asn	Glu	Pro	Leu	Ala	Pro	Asp	Glu	Val	Leu	Leu	Ala	Pro
			85						90					95	
Arg	Thr	Glu	Thr	Ala	Glu	Ser	Thr	Pro	Ser	Trp	Gln	Val	Leu	Lys	Leu
			100					105						110	
Val	Phe	Cys	Ala	Ser	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Ile
		115					120					125			
Leu	Gln	Glu	Arg	Val	Met	Thr	Gly	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser
	130					135					140				
Pro	Gly	Glu	His	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg
145					150					155					160
Val	Leu	Ala	Leu	Val	Val	Ala	Gly	Leu	Tyr	Cys	Val	Leu	Arg	Lys	Gln
			165						170					175	
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser
			180					185					190		
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser
		195					200					205			
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met
	210					215					220				
Met	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr
225					230					235					240
Leu	Thr	Ala	Gly	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser
			245						250					255	
Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	Gly	Leu
			260					265					270		
Val	Leu	Leu	Ala	Gly	Tyr	Ile	Ala	Phe	Asp	Ser	Phe	Thr	Ser	Asn	Trp
			275				280					285			
Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Lys	Met	Ser	Ser	Val	Gln	Met	Met	Phe
	290					295					300				
Gly	Val	Asn	Leu	Phe	Ser	Cys	Leu	Phe	Thr	Val	Gly	Ser	Leu	Leu	Glu
305					310					315					320
Gln	Gly	Ala	Leu	Glu	Gly	Ala	Arg	Phe	Met	Gly	Arg	His	Ser	Glu	
			325					330					335		
Phe	Ala	Leu	His	Ala	Leu	Leu	Leu	Ser	Ile	Cys	Ser	Ala	Phe	Gly	Gln
			340					345					350		
Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly	Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr
		355					360					365			
Ile	Ile	Met	Thr	Leu	Arg	Gln	Ala	Ile	Ala	Ile	Leu	Leu	Ser	Cys	Leu
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<210> 342
<211> 51
<212> PRT
<213> Mouse
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<400> 342  
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                   20                  25                  30  
 Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His Leu Thr Leu Thr  
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 Ser Tyr Ala  
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<210> 343  
 <211> 51  
 <212> PRT  
 <213> Human  
 <400> 343

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                   20                  25                  30  
 Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu His Leu Thr Leu Thr  
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 Ser Tyr Ala  
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<210> 344  
 <211> 95  
 <212> PRT  
 <213> Human

<400> 344  
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 Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr  
                   20                  25                  30  
 Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu  
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 Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly  
                   50                  55                  60  
 Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile  
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 Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
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<210> 345  
 <211> 77  
 <212> PRT  
 <213> Mouse

<400> 345  
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 Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu  
                   35                  40                  45  
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp  
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Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
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<210> 346  
<211> 77  
<212> PRT  
<213> Human

<400> 346

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp  
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Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu  
35 40 45  
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp  
50 55 60  
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
65 70 75

<210> 347  
<211> 215  
<212> PRT  
<213> Mouse

<400> 347

Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys  
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Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser  
20 25 30  
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser  
35 40 45  
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val  
50 55 60  
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu  
65 70 75 80  
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn  
85 90 95  
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe  
100 105 110  
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn  
115 120 125  
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val  
130 135 140  
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser  
145 150 155 160  
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala  
165 170 175  
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala  
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195 200 205  
Lys Ser Leu Ala Ile Arg Thr  
210 215

<210> 348  
<211> 21



<212> PRT  
<213> Mouse

<400> 348  
Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly Ser Lys Val  
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Pro Gln Phe Leu Asn

<210> 349  
<211> 417  
<212> DNA  
<213> Mouse

<400> 349  
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ctgcaccccg aggtgcctgg cctctacaac tacctgccgt ggcagtacca agctggagag 360  
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<210> 350  
<211> 1837  
<212> DNA  
<213> Mouse

<400> 350  
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tctcacagca tcgggaaggg gagcttcgag aggtccaagc gcttcgcat cgctgcctgt 360  
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cctcatctgg aattcccctt ggactccttc tcaactcgac aggaagtga ggaagcatc 480  
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ccgaaggacc ggcagtgtgt gttggctgag caagtggagg atgccacaa tggcctcctc 780  
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<210> 351  
 <211> 941  
 <212> DNA  
 <213> Mouse

<400> 351						
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aatgaagttg	atctaccagg	gtcggctgct	gcaggaccca	gcacgcacac	tgagttccct	900
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<210> 352  
 <211> 571  
 <212> DNA  
 <213> Mouse

<400> 352						
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tatgggaatg	tcagggtctc	ctcaccttga	cagctgataa	ttccattcct	cgactcttga	540
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<210> 353  
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 <212> DNA  
 <213> Rat

<400> 353						
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&lt;210&gt; 354

&lt;211&gt; 528

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 354

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gccctatagc	cagaggagt	ccctggctaa	ctgcagtggt	agcttgtaag	caacagaagt	480
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&lt;210&gt; 355

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 355

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&lt;210&gt; 356

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 356

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&lt;210&gt; 357

&lt;211&gt; 1206

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 357

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&lt;210&gt; 358

&lt;211&gt; 1052

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 358

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&lt;210&gt; 359

&lt;211&gt; 1134

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 359

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&lt;210&gt; 360

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 360

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&lt;210&gt; 361

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 361

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&lt;210&gt; 362

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 362

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 <212> DNA  
 <213> Mouse

<400> 363						
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 <212> DNA  
 <213> Mouse

<400> 364						
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 <212> DNA  
 <213> Rat

<400> 365						
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<210> 366  
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&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 366

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&lt;210&gt; 367

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 367

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&lt;210&gt; 368

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 368

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&lt;210&gt; 369

&lt;211&gt; 824

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 369

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 <212> DNA  
 <213> Mouse

<400> 370						
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 <212> DNA  
 <213> Human

<400> 371						
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<210> 372  
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&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 372

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&lt;210&gt; 373

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 373

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Met Pro Leu Pro Leu Leu Leu Ala Ala Leu Cys Leu Ala Ala Ser Pro
1          5          10          15
Ala Pro Ala Arg Ala Cys Gln Leu Pro Ser Glu Trp Arg Pro Leu Ser
20          25          30
Glu Gly Cys Arg Ala Glu Leu Ala Glu Thr Ile Val Tyr Ala Lys Val
35          40          45
Leu Ala Leu His Pro Glu Val Pro Gly Leu Tyr Asn Tyr Leu Pro Trp

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50                      55                      60  
 Gln Tyr Gln Ala Gly Glu Gly Gly Leu Phe Tyr Ser Ala Glu Val Glu  
 65                      70                      75                      80  
 Met Leu Val

<210> 374  
 <211> 405  
 <212> PRT  
 <213> Mouse

<400> 374  
 Met Pro Pro Leu Leu Leu Pro Ala Ile Tyr Met Leu Leu Phe Phe  
 1                      5                      10                      15  
 Arg Val Ser Pro Thr Ile Ser Leu Gln Glu Val His Val Asn Arg Glu  
                     20                      25                      30  
 Thr Met Gly Lys Ile Ala Val Ala Ser Lys Leu Met Trp Cys Ser Ala  
                     35                      40                      45  
 Ala Val Asp Ile Leu Phe Leu Leu Asp Gly Ser His Ser Ile Gly Lys  
                     50                      55                      60  
 Gly Ser Phe Glu Arg Ser Lys Arg Phe Ala Ile Ala Ala Cys Asp Ala  
 65                      70                      75                      80  
 Leu Asp Ile Ser Pro Gly Arg Val Arg Val Gly Ala Leu Gln Phe Gly  
                     85                      90                      95  
 Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Arg Gln  
                     100                      105                      110  
 Glu Val Lys Glu Ser Ile Lys Gly Ile Val Phe Lys Gly Gly Arg Thr  
                     115                      120                      125  
 Glu Thr Gly Leu Ala Leu Lys Arg Leu Ser Arg Gly Phe Pro Gly Gly  
                     130                      135                      140  
 Arg Asn Gly Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly Lys  
 145                      150                      155                      160  
 Ser Gln Gly Pro Val Ala Leu Pro Ala Lys Gln Leu Arg Glu Arg Gly  
                     165                      170                      175  
 Ile Val Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Asp Glu Leu  
                     180                      185                      190  
 Leu Thr Leu Ala Ser Glu Pro Lys Asp Arg His Val Leu Leu Ala Glu  
                     195                      200                      205  
 Gln Val Glu Asp Ala Thr Asn Gly Leu Leu Ser Thr Leu Ser Ser Ser  
                     210                      215                      220  
 Ala Leu Cys Thr Thr Ala Asp Pro Asp Cys Arg Val Glu Pro His Pro  
 225                      230                      235                      240  
 Cys Glu Arg Arg Thr Leu Glu Thr Val Arg Glu Leu Ala Gly Asn Ala  
                     245                      250                      255  
 Leu Cys Trp Arg Gly Ser Arg Gln Ala Asp Thr Val Leu Ala Leu Pro  
                     260                      265                      270  
 Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Gln Thr His Pro Ala Asn  
                     275                      280                      285  
 Cys Tyr Arg Thr Ile Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys Gln  
                     290                      295                      300  
 Asn Gly Gly Thr Cys Ile Pro Glu Gly Val Asp Arg Tyr His Cys Leu  
 305                      310                      315                      320  
 Cys Pro Leu Ala Phe Gly Gly Glu Val Asn Cys Ala Pro Lys Leu Ser  
                     325                      330                      335  
 Leu Glu Cys Arg Ile Asp Val Leu Phe Leu Leu Asp Ser Ser Ala Gly  
                     340                      345                      350  
 Thr Thr Leu Gly Gly Phe Arg Arg Ala Lys Ala Phe Val Lys Arg Phe

355				360				365							
Val	Gln	Ala	Val	Leu	Arg	Glu	Asp	Ser	Arg	Ala	Arg	Val	Gly	Ile	Ala
370				375				380							
Ser	Tyr	Gly	Arg	Asn	Leu	Met	Val	Ala	Val	Pro	Cys	Arg	Gly	Val	Pro
385				390				395				400			
Ala	Leu	Cys	Arg	Thr											
405															

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<210> 375
<211> 180
<212> PRT
<213> Mouse
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[illegible]

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<210> 376
<211> 68
<212> PRT
<213> Mouse
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	<400>	376																		
Met	Cys	Leu	Pro	Val	Thr	Val	Trp	Cys	His	Trp	Ala	Leu	Trp	Val	Ala					
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His	Leu	Pro	Leu	Ile	Pro	Ser	Val	Gly	Lys	Ser	Gln	Cys	Thr	Gln	Met					
			20					25						30						
Trp	His	Cys	Cys	Met	Pro	Trp	Val	Cys	Val	Gly	Asp	Cys	Leu	Cys	Leu					
		35					40					45								
Ser	Asp	Pro	Leu	Trp	Leu	Cys	Leu	Leu	Lys	Glu	Thr	Glu	Thr	Pro	Cys					
	50					55					60									
Gly	Phe	Leu	Ser																	
65																				

<210> 377

<211> 107  
 <212> PRT  
 <213> Rat

<400> 377  
 Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Val Cys Val Leu Leu  
 1 5 10 15  
 Pro Leu His His Gly Ala Pro Gly Pro Glu Gly Thr Ala Pro Asp Pro  
 20 25 30  
 Ala His Tyr Arg Glu Arg Val Lys Ala Met Phe Tyr His Ala Tyr Asp  
 35 40 45  
 Ser Tyr Leu Glu Asn Ala Phe Pro Tyr Asp Glu Leu Arg Pro Leu Thr  
 50 55 60  
 Cys Asp Gly His Asp Thr Trp Gly Ser Phe Ser Leu Thr Leu Ile Asp  
 65 70 75 80  
 Ala Leu Asp Thr Leu Leu Ile Leu Gly Asn Thr Ser Glu Phe Gln Arg  
 85 90 95  
 Val Val Glu Val Leu Gln Asp Lys Arg Gly Leu  
 100 105

<210> 378  
 <211> 95  
 <212> PRT  
 <213> Rat

<400> 378  
 Met Trp Phe Leu Pro Cys Ser Val Pro Leu Val Ile Ser Ser Cys His  
 1 5 10 15  
 Ser Gln Ala Ser Pro His Trp Pro Tyr Gly Ile Ile Ser Gly Gly Gln  
 20 25 30  
 Glu Gly Leu Cys Arg Leu Trp Thr Ala Thr Cys His Ser Arg Gly Glu  
 35 40 45  
 Ser Glu Val Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln  
 50 55 60  
 Gly Ser Leu Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys  
 65 70 75 80  
 Ala His Thr Ser Met Asp Arg Thr Leu Gly Leu Leu Ser Cys Cys  
 85 90 95

<210> 379  
 <211> 138  
 <212> PRT  
 <213> Mouse

<400> 379  
 Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu  
 1 5 10 15  
 Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser  
 20 25 30  
 Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met  
 35 40 45  
 Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe  
 50 55 60  
 Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe  
 65 70 75 80  
 Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys  
 85 90 95

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr  
 100 105 110  
 Arg Ser Ser Leu Asp Asp Leu Ser Ile Val Gly Gln Val Lys Arg Ile  
 115 120 125  
 His Gln Phe Val Glu Cys Leu Lys Leu Asn  
 130 135

<210> 380

<211> 81

<212> PRT

<213> Rat

<400> 380

Met Ala Ser Ser Asn Trp Leu Ser Gly Val Asn Val Val Leu Val  
 1 5 10 15  
 Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe Ile Phe Val Lys  
 20 25 30  
 Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg Gly Pro His Val  
 35 40 45  
 Pro Val Gly His Asn Ala Pro Lys Asp Leu Lys Glu Glu Ile Asp Ile  
 50 55 60  
 Arg Leu Ser Arg Val Gln Asp Ile Lys Tyr Glu Pro Gln Leu Leu Ala  
 65 70 75 80  
 Asp

<210> 381

<211> 257

<212> PRT

<213> Mouse

<400> 381

Met Arg Ser Gly Ala Leu Trp Pro Leu Leu Trp Gly Ala Leu Val Trp  
 1 5 10 15  
 Thr Val Gly Ser Val Gly Ala Val Met Gly Ser Glu Asp Ser Val Pro  
 20 25 30  
 Gly Gly Val Cys Trp Leu Gln Gln Gly Arg Glu Ala Thr Cys Ser Leu  
 35 40 45  
 Val Leu Lys Thr Arg Val Ser Arg Glu Glu Cys Cys Ala Ser Gly Asn  
 50 55 60  
 Ile Asn Thr Ala Trp Ser Asn Phe Thr His Pro Gly Asn Lys Ile Ser  
 65 70 75 80  
 Leu Leu Gly Phe Leu Gly Leu Val His Cys Leu Pro Cys Lys Asp Ser  
 85 90 95  
 Cys Asp Gly Val Glu Cys Gly Pro Gly Lys Ala Cys Arg Met Leu Gly  
 100 105 110  
 Gly Arg Pro Thr Leu Arg Ser Cys Val Pro Asn Cys Glu Gly Leu Pro  
 115 120 125  
 Ala Gly Phe Gln Val Cys Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu  
 130 135 140  
 Cys Glu Leu Arg Thr Ala Arg Cys Arg Gly His Pro Asp Leu Arg Val  
 145 150 155 160  
 Met Tyr Arg Gly Arg Cys Gln Lys Ser Cys Ala Gln Val Val Cys Pro  
 165 170 175  
 Arg Pro Gln Ser Cys Leu Val Asp Gln Thr Gly Ser Ala His Cys Val  
 180 185 190  
 Val Cys Arg Ala Ala Pro Cys Pro Val Pro Ser Asn Pro Gly Gln Glu

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      195              200              205
Leu Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Leu Arg
 210              215              220
Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Pro Gly
 225              230              235              240
Ile Cys Thr Gly Gly Pro Lys Val Pro Ala Glu Glu Glu Glu Asn Phe
      245              250              255
Val

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&lt;210&gt; 382

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 382

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Met Ile Ser Trp Met Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
 1              5              10              15
Pro Met Leu Gly Ala Phe Ala Arg Arg Asp Phe Gln Lys Gly Gly Pro
      20              25              30
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
 35              40              45
Gly Ala Pro Gly Ser Ser Gly Met Val Gly Arg Met Gly Phe Pro Gly
 50              55              60
Lys Asp Gly Gln Asp Gly Gln Asp Gly Asp Arg Gly Asp Ser Gly Glu
 65              70              75              80
Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Gln Gly Pro Lys
      85              90              95
Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly
 100              105              110
Val Ser Gly Thr Pro Gly Lys His Gly Ile Pro Gly Lys Lys Gly Pro
 115              120              125
Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly
 130              135              140
Ser Ser Arg Ala Lys Ser Ala Phe Ser Val Ser Val Thr Lys Ser Tyr
 145              150              155              160
Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu
      165              170              175
Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Ser Val Pro
 180              185              190
Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu
 195              200              205
Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp
 210              215              220
Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala
 225              230              235              240
Leu Lys Glu Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln
      245              250              255
Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly
 260              265              270
Phe Leu Ile Tyr Ala Asp Gln Gly Asp Pro Asn Glu Val
      275              280              285

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&lt;210&gt; 383

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Rat

<400> 383  
 Met Lys Leu Leu Cys Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
 1 5 10 15  
 Pro Ala Gln Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
 20 25 30  
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
 35 40 45  
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
 50 55 60  
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr  
 65 70 75 80  
 Glu Glu Arg Ser Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu  
 85 90 95  
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val  
 100 105 110  
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
 115 120 125  
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser  
 130 135 140  
 Ile Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
 145 150 155 160  
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
 165 170 175  
 Asp Arg His Lys Met Leu Ser  
 180

<210> 384  
 <211> 292  
 <212> PRT  
 <213> Mouse

<400> 384  
 Cys Gln Leu Pro Leu Arg Val Leu Ile Ile Ser Asn Asn Lys Leu Gly  
 1 5 10 15  
 Ala Leu Pro Pro Asp Ile Ser Thr Leu Gly Ser Leu Arg Gln Leu Asp  
 20 25 30  
 Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Val Glu Leu Cys Ser Leu  
 35 40 45  
 Arg Ser Leu Arg Asp Leu Asn Val Arg Arg Asn Gln Leu Ser Thr Leu  
 50 55 60  
 Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Arg Leu Asp Phe Ser Cys  
 65 70 75 80  
 Asn Arg Ile Ser Arg Ile Pro Val Ser Phe Cys Arg Leu Arg His Leu  
 85 90 95  
 Gln Val Val Leu Leu Asp Ser Asn Pro Leu Gln Ser Pro Pro Ala Gln  
 100 105 110  
 Ile Cys Leu Lys Gly Lys Leu His Ile Phe Lys Tyr Leu Thr Met Glu  
 115 120 125  
 Ala Gly Arg Arg Gly Ala Ala Leu Gly Asp Leu Val Pro Ser Arg Pro  
 130 135 140  
 Pro Ser Phe Ser Pro Cys Pro Ala Glu Asp Leu Phe Pro Gly Arg Arg  
 145 150 155 160  
 Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser Gly Ser  
 165 170 175  
 Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu Leu Ser  
 180 185 190



Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg Gln Pro  
 195 200 205  
 Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp Phe Ile  
 210 215 220  
 Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala Glu Glu  
 225 230 235 240  
 Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu Lys Pro  
 245 250 255  
 Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg Arg Pro  
 260 265 270  
 Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln Gln  
 275 280 285  
 Ser Gly Gly Trp  
 290

<210> 385  
 <211> 164  
 <212> PRT  
 <213> Mouse

<400> 385  
 Ser Arg Gln Leu Arg Ala Pro Arg Phe Asp Pro Arg Ala Gly Phe His  
 1 5 10 15  
 Ala Glu Gly Lys Asp Arg Gly Pro Ser Val Pro Gln Gly Leu Leu Lys  
 20 25 30  
 Ala Ala Arg Ser Ser Gly Gln Leu Asn Leu Ala Gly Arg Asn Leu Gly  
 35 40 45  
 Glu Val Pro Gln Cys Val Trp Arg Ile Asn Val Asp Ile Pro Glu Glu  
 50 55 60  
 Ala Asn Gln Asn Leu Ser Phe Ser Ser Thr Glu Arg Trp Trp Asp Gln  
 65 70 75 80  
 Thr Asp Leu Thr Lys Leu Ile Ile Ser Ser Asn Lys Leu Gln Ser Leu  
 85 90 95  
 Ser Asp Asp Leu Arg Leu Leu Pro Ala Leu Thr Val Leu Asp Ile His  
 100 105 110  
 Asp Asn Gln Leu Thr Ser Leu Pro Ser Ala Ile Arg Glu Leu Asp Asn  
 115 120 125  
 Leu Gln Lys Leu Asn Val Ser His Asn Lys Leu Lys Ile Leu Pro Glu  
 130 135 140  
 Glu Ile Thr Ser Leu Lys Asn Leu Arg Thr Leu His Leu Gln His Asn  
 145 150 155 160  
 Glu Leu Thr Cys

<210> 386  
 <211> 71  
 <212> PRT  
 <213> Mouse

<400> 386  
 Ser Leu Ser Ile Leu Pro Ala Val Arg Val Ser Pro Arg Pro Thr Tyr  
 1 5 10 15  
 Pro Ser Thr Ala Ser Ser Met Ala Ala Phe Leu Val Thr Gly Phe Phe  
 20 25 30  
 Phe Ser Leu Phe Val Val Leu Gly Met Glu Pro Arg Ala Leu Phe Arg  
 35 40 45  
 Pro Asp Lys Ala Leu Pro Leu Ser Cys Ala Lys Pro Thr Ser Leu Cys

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      50      55      60
Val Gln Ser Ser Phe Leu Gly
65      70

<210> 387
<211> 126
<212> PRT
<213> Mouse

<400> 387
Glu Tyr Glu Ala Arg Val Leu Glu Lys Ser Leu Arg Lys Glu Ser Arg
 1      5      10      15
Asn Lys Glu Thr Asp Lys Val Lys Leu Thr Trp Arg Asp Arg Phe Pro
 20      25      30
Ala Tyr Phe Thr Asn Leu Val Ser Ile Ile Phe Met Ile Ala Val Thr
 35      40      45
Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg Ile Ser Thr Ala Ala
 50      55      60
Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg Ser Asn Ile Arg Val
 65      70      75      80
Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu Val Val Ile Ile Leu
 85      90      95
Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp Leu Thr Lys Ile Gly
100      105      110
Glu Cys His Val Gln Asp Ser Ile Gly Ser Met Gly Leu Gly
115      120      125

<210> 388
<211> 84
<212> PRT
<213> Rat

<400> 388
Ala Ala Glu Asn Glu Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser
 1      5      10      15
Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly Phe Val Met Gly Cys
 20      25      30
Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu
 35      40      45
Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr
 50      55      60
Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met
 65      70      75      80
Gly Ile Arg Cys

<210> 389
<211> 284
<212> PRT
<213> Rat

<400> 389
Gly Gly Ser Ser Val Ser His Val Leu Arg Gly Ser Gly Gln Glu Arg
 1      5      10      15
Ser Pro Pro Pro Ala Ser Met Gln Pro Pro Trp Gly Leu Ala Leu Pro
 20      25      30
Leu Leu Leu Pro Trp Val Ala Gly Gly Val Gly Thr Ser Pro Arg Asp

```

```

      35      40      45
Tyr Trp Leu Pro Ala Leu Ala His Gln Pro Gly Val Cys His Tyr Gly
  50      55      60
Thr Lys Thr Ala Cys Cys Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val
  65      70      75      80
Cys Glu Ala Val Cys Glu Pro Arg Cys Lys Phe Gly Glu Cys Val Gly
      85      90      95
Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser
      100      105      110
Gln Asp Val Asn Glu Cys Ala Phe Lys Pro Arg Pro Cys Gln His Arg
      115      120      125
Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His
      130      135      140
Met Leu Leu Pro Asp Ala Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg
      145      150      155      160
Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys
      165      170      175
Val Cys Pro Ser Ser Gly Leu Arg Leu Gly Pro Asn Gly Arg Val Cys
      180      185      190
Leu Asp Ile Asp Glu Cys Ala Ser Ser Lys Ala Val Cys Pro Ser Asn
      195      200      205
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile
      210      215      220
Gly Phe Glu Leu Lys Tyr Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile
      225      230      235      240
Asn Glu Cys Thr Leu Asn Thr Arg Thr Cys Ser Pro His Ala Asn Cys
      245      250      255
Leu Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg
      260      265      270
Gly Asn Gly Leu Gln Cys Ser Val Ile Pro Glu His
      275      280

```

<210> 390  
 <211> 85  
 <212> PRT  
 <213> Rat

```

      <400> 390
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
  1      5      10      15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
      20      25      30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
      35      40      45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
      50      55      60
Pro Gln Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
      65      70      75      80
Gln Thr Asn Ile Leu
      85

```

<210> 391  
 <211> 158  
 <212> PRT  
 <213> Rat

<400> 391

```

Phe Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser
1      5      10      15
Glu Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln
20      25      30
Leu Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu
35      40      45
Gly Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala
50      55      60
Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
65      70      75      80
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
85      90      95
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
100     105     110
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
115     120     125
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
130     135     140
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu
145     150     155

```

```

<210> 392
<211> 124
<212> PRT
<213> Mouse

```

```

<400> 392
Ala Ala Glu Gln Glu Ala Ser Ser Arg Arg Arg Gly Gly Ala Gly
1      5      10      15
Pro Ala Leu Phe Ser Ser Gly Ser Leu Arg Ser Glu Pro Gln Pro Arg
20      25      30
Leu Pro Gln Ala Arg Ser Arg Pro Arg Pro Ser Phe Leu Gln Ala Arg
35      40      45
Ser Arg Pro Cys Leu Ser Gln Ala Cys Ser Pro Ala Ala Ser Val Leu
50      55      60
Ser Ser Ser Ser Leu Cys Gly Arg Ser His Leu Leu Pro Gly Ser Leu
65      70      75      80
Pro Ala Thr Ala Phe Leu Leu Leu Leu Pro Gly Ser Leu Pro Gly Arg
85      90      95
Arg Pro Ser Ala Ala Gln Ala Ala Pro Val Leu Ala Trp Gly Leu Val
100     105     110
Ala Phe Gln Leu Gly Val Ala Ala Gly Ala Gly Arg
115     120

```

```

<210> 393
<211> 242
<212> PRT
<213> Rat

```

```

<400> 393
Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
1      5      10      15
Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
20      25      30
Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
35      40      45
Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys

```

```

      50      55      60
Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
65      70      75      80
Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
      85      90      95
Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Pro Cys Lys
      100      105      110
Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
      115      120      125
Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
      130      135      140
Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
      145      150      155      160
Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
      165      170      175
Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
      180      185      190
Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
      195      200      205
Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
      210      215      220
Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
      225      230      235      240
Gly Arg

```

<210> 394  
 <211> 99  
 <212> PRT  
 <213> Mouse

```

      <400> 394
Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
1      5      10      15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
      20      25      30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
      35      40      45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
      50      55      60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
      65      70      75      80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
      85      90      95
Tyr Glu Glu

```

<210> 395  
 <211> 103  
 <212> PRT  
 <213> Human

```

      <400> 395
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
1      5      10      15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
      20      25      30

```

Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile  
                   35                  40                  45  
 Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His  
                   50                  55                  60  
 Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu  
                   65                  70                  75                  80  
 Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys  
                   85                  90                  95  
 Ser Gly Glu Arg Arg Pro Leu  
                   100

<210> 396

<211> 1529

<212> PRT

<213> Rat

<400> 396

Met Ser Gly Ile Gly Trp Gln Thr Leu Ser Leu Ser Leu Ala Leu Val  
   1                  5                  10                  15  
 Leu Ser Ile Leu Asn Lys Val Ala Pro His Ala Cys Pro Ala Gln Cys  
                   20                  25                  30  
 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser  
                   35                  40                  45  
 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly  
                   50                  55                  60  
 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His  
                   65                  70                  75                  80  
 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg  
                   85                  90                  95  
 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg  
                   100                  105                  110  
 Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys  
                   115                  120                  125  
 Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg  
                   130                  135                  140  
 Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr  
                   145                  150                  155                  160  
 Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp  
                   165                  170                  175  
 Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val  
                   180                  185                  190  
 Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser  
                   195                  200                  205  
 Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu  
                   210                  215                  220  
 Arg Gln Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser  
                   225                  230                  235                  240  
 His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val  
                   245                  250                  255  
 Cys Ser Gly His Gln Ser Phe Met Ala Pro Ser Cys Ser Val Leu His  
                   260                  265                  270  
 Cys Pro Ile Ala Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly  
                   275                  280                  285  
 Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu Thr Ile Thr Glu  
                   290                  295                  300  
 Ile Arg Leu Glu Gln Asn Ser Ile Arg Val Ile Pro Pro Gly Ala Phe  
                   305                  310                  315                  320

Ser Pro Tyr Lys Lys Leu Arg Arg Leu Asp Leu Ser Asn Asn Gln Ile  
 325 330 335  
 Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg Ser Leu Asn Ser  
 340 345 350  
 Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro Lys Ser Leu Phe  
 355 360 365  
 Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn Ala Asn Lys Ile  
 370 375 380  
 Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His Asn Leu Asn Leu  
 385 390 395  
 Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Val Ala Lys Gly Thr Phe  
 405 410 415  
 Ser Ala Leu Arg Ala Ile Gln Thr Met His Leu Ala Gln Asn Pro Phe  
 420 425 430  
 Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr Leu His Thr Asn  
 435 440 445  
 Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro Arg Arg Leu Ala  
 450 455 460  
 Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe Arg Cys Ser Ala  
 465 470 475  
 Lys Glu Gln Tyr Phe Ile Pro Gly Thr Glu Asp Tyr Arg Ser Lys Leu  
 485 490 495  
 Ser Gly Asp Cys Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys  
 500 505 510  
 Glu Gly Thr Thr Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro  
 515 520 525  
 Asp His Ile Pro Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu  
 530 535 540  
 Phe Thr Val Leu Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu  
 545 550 555  
 Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly  
 565 570 575  
 Ala Phe Glu Gly Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn  
 580 585 590  
 Arg Leu Glu Asn Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu  
 595 600 605  
 Lys Thr Leu Met Leu Arg Ser Asn Arg Ile Ser Cys Val Gly Asn Asp  
 610 615 620  
 Ser Phe Thr Gly Leu Gly Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn  
 625 630 635  
 Gln Ile Thr Thr Val Ala Pro Gly Ala Phe Gly Thr Leu His Ser Leu  
 645 650 655  
 Ser Thr Leu Asn Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys His Leu  
 660 665 670  
 Ala Trp Leu Gly Glu Trp Leu Arg Arg Lys Arg Ile Val Thr Gly Asn  
 675 680 685  
 Pro Arg Cys Gln Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp  
 690 695 700  
 Val Ala Ile Gln Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser  
 705 710 715  
 Cys Ser Pro Leu Ser Arg Cys Pro Ser Glu Cys Thr Cys Leu Asp Thr  
 725 730 735  
 Val Val Arg Cys Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile  
 740 745 750  
 Pro Arg Asp Val Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu  
 755 760 765  
 Val Pro Lys Glu Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu

770		775		780
Ser Asn Asn Arg Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met				
785		790		795
Thr Gln Leu Leu Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile				
	805		810	815
Pro Pro Arg Thr Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu				
	820		825	830
His Gly Asn Asp Ile Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu				
	835		840	845
Ser Ala Leu Ser His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp				
	850		855	860
Cys Asn Met Gln Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu				
865		870		875
Pro Gly Ile Ala Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu				
	885		890	895
Leu Leu Thr Thr Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp				
	900		905	910
Val Thr Ile Gln Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys				
	915		920	925
Asn Asp Gly Thr Cys Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr				
	930		935	940
Cys Pro Tyr Gly Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala				
945		950		955
Cys Ile Ser Asn Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu				
	965		970	975
Gly Glu Asn Asp Gly Phe Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly				
	980		985	990
Glu Ser Cys Asp Ile Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu				
	995		1000	1005
Asn Asn Ser Thr Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys				
	1010		1015	1020
Pro Pro Glu Tyr Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys				
1025		1030		1035
Ala Gln Asp Leu Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr				
	1045		1050	1055
Pro Lys Gly Phe Lys Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His				
	1060		1065	1070
Cys Asp Ile Asp Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly				
	1075		1080	1085
Ala His Cys Thr Asp Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu				
	1090		1095	1100
Gly Tyr Ser Gly Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Leu				
1105		1110		1115
Arg Thr Ser Pro Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys				
	1125		1130	1135
Ile Ile Arg Val Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu				
	1140		1145	1150
Gly Glu Lys Cys Glu Lys Leu Val Ser Val Asn Phe Val Asn Lys Glu				
	1155		1160	1165
Ser Tyr Leu Gln Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile				
	1170		1175	1180
Thr Leu Gln Ile Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys				
1185		1190		1195
Gly Asp Lys Asp His Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg				
	1205		1210	1215
Ala Ser Tyr Asp Thr Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val				
	1220		1225	1230



Glu Thr Ile Asn Asp Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu  
 1235 1240 1245  
 Asp Ser Ser Leu Ser Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile  
 1250 1255 1260  
 Thr Asn Leu Ser Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr  
 1265 1270 1275 128  
 Val Gly Gly Met Pro Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala  
 1285 1290 1295  
 Pro Gly Gln Asn Gly Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr  
 1300 1305 1310  
 Ile Asn Ser Glu Leu Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly  
 1315 1320 1325  
 Ile Leu Pro Gly Cys Glu Pro Cys His Lys Lys Val Cys Ala His Gly  
 1330 1335 1340  
 Thr Cys Gln Pro Ser Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu  
 1345 1350 1355 136  
 Gly Trp Met Gly Pro Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu  
 1365 1370 1375  
 Gly Asn Lys Cys Val His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser  
 1380 1385 1390  
 Tyr Ser Cys Lys Cys Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu  
 1395 1400 1405  
 Glu Glu Asp Leu Phe Asn Pro Cys Gln Val Ile Lys Cys Lys His Gly  
 1410 1415 1420  
 Lys Cys Arg Leu Ser Gly Leu Gly Gln Pro Tyr Cys Glu Cys Ser Ser  
 1425 1430 1435 144  
 Gly Phe Thr Gly Asp Ser Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu  
 1445 1450 1455  
 Arg Ile Arg Asp Tyr Tyr Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln  
 1460 1465 1470  
 Thr Thr Lys Lys Val Ser Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly  
 1475 1480 1485  
 Gly Gln Cys Cys Gly Pro Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe  
 1490 1495 1500  
 Glu Cys Thr Asp Gly Ser Ser Phe Val Asp Glu Val Glu Lys Val Val  
 1505 1510 1515 152  
 Lys Cys Gly Cys Thr Arg Cys Ala Ser  
 1525

<210> 397  
 <211> 8  
 <212> PRT  
 <213> Mouse

<400> 397  
 Trp Tyr Asn Ala Trp Asn Glu Lys  
 1 5

<210> 398  
 <211> 7  
 <212> PRT  
 <213> Mouse

<400> 398  
 Met Val Ile Ile Thr Thr Lys  
 1 5

<210> 399  
 <211> 2206  
 <212> DNA  
 <213> Rat

<400> 399  
 gtttcgtctt aacgccctct ctgctgttggc agaactggcc gtgggctccc gctggtacca 60  
 tggaaacatct cagcccacac agactaagcg gagactgatg ttggtggcgt tcctcggagc 120  
 atccgcgggtg actgcaagta ccggtctcct gtggaagaag gctcacgcag aatctccacc 180  
 gagcgtcaac agcaagaaga ctgacgctgg agataagggg aagagcaagg acaccggga 240  
 agtgtccagc catgaaggaa gcgctgcaga cactcgggcc gagccttacc cagaggagaa 300  
 gaagaagaag cgttctggat tcagagacag aaaagtaatg gagtatgaga ataggatccg 360  
 agcctactcc acaccagaca aaatcttccg gtattttgcc accttgaaag taatcaacga 420  
 acctggtgaa actgaagtgt tcatgacccc acaggacttt gtgcgctcca taacacccaa 480  
 tgagaagcag ccagaacact tgggcctgga tcagtacata ataaagcgct tcgatggaaa 540  
 gaaaatttggc caggaaacgag aaaagtttgc tgacgaaggc agcatcttct atacccttgg 600  
 agagtgtgga ctcatctcct tctctgacta catcttctct acaacgggtgc tctccactcc 660  
 tcagagaaat ttctgaaattg ccttcaagat gtttgacttg aatggagatg gagaagtaga 720  
 catggaggag tttgagcagg ttcaaagcat cattcgctcc cagaccagca tgggcatgag 780  
 tcacagagat cgtccaacta ctgggaacac cctcaagtct ggcttatgtt cggccctcac 840  
 gacctacttt tttggagctg atctcaaaag gaaactgacc attaaaaact tcctggaatt 900  
 tcagcgtaaa ctgcagcatg acgttctaaa gctggagtgt gaacgccatg acccggtaga 960  
 cgggagaatc tctgagaggc agttcgggtg catgctgctg gcctacagtg gagtgcagtc 1020  
 caagaagctg accgccatgc agaggcagct gaagaagcac ttcaaggatg ggaagggcct 1080  
 gactttccag gaggtggaga acttcttcac tttcctgaag aacattaatg acgtggacac 1140  
 tcgcttaagc ttttaccaca tggctggagc atccctcgat aaagtgacca tgcagcaagt 1200  
 ggccaggaca gtggcgaaag tctgagctgtc ggaccacgtg tgtgacgtgg tgtttgcact 1260  
 ctttgactgc gacggcaatg gggagctgag caataaggag tttgtctcca tcatgaagca 1320  
 gcggctgatg agaggcctgg agaagcccaa ggacatgggc tttaccctgc tcacgcaggc 1380  
 catgtggaaa tgtgcccaag aaaccgectg ggactttgct ctaccctaat agtaccctac 1440  
 ctctcgcacc ttagcaccac gcaatcctgg agtggccttc atgctgctga tgcctctggg 1500  
 agtagtgccc acatcccatc ctttctggaa gtgacctctg gcctcagctg gctgacctct 1560  
 ccactctccc ctgaccagct cagtgttccg ctaggctctg aatctgcagt cagatcaaa 1620  
 gtctaagaca ggaacaagtc ttcaaagcag agaccatagc tcccttaacc agtgccctg 1680  
 gggtaaatgc ggggagccct ccacactggc cagccccagg aggcattctc gcagtctctc 1740  
 actgtggatt taagtaacac aaacgtccct gccatcttcc tcccactgtt ttaaagctgc 1800  
 aagtttggaa atactctggc aggcacaggg aagtctgtga tgaacggtaa tgcagatgac 1860  
 cctggtaccc tgatctggca gggcacctgg tcagggggag ggtctgcgtc agacaccagc 1920  
 ggcaccagga aggcctcttg ccaccagcac agctcccgat tcaaagtcgc tgctttgagc 1980  
 ggctctccag aacctcctgc tctttttttt ttctctcccg ctccctgcga tgcctctctc 2040  
 gggactctgc ttactagag ccagggtgta gccctgttcc cttgtgtctt gtccctctct 2100  
 tatagacctg cagagcgag ctcagagcct atctgcctc tgtctaatac actcgtaaat 2160  
 atcactttta ttatagcact ttgcaggaaa taccctaaaa aaaaaa 2206

<210> 400  
 <211> 160  
 <212> DNA  
 <213> Mouse

<400> 400  
 tcgcaggacg ctactgggac agcttgggct ttttccagtt gattttatgg tttgcatctt 60  
 tctctttctc tttttctggt tcttgttccc ctttcccttt ttcttggtga gaaagcacat 120  
 attactgagc cattgcaagg aatgggaggg gtccacaatg 160

<210> 401  
 <211> 430  
 <212> DNA

&lt;213&gt; Rat

&lt;400&gt; 401

ggcaccagcc	cggtctctgt	gtctccgtca	gtctccagcg	atccctccct	acctccgccc	60
tccatggcgt	cgctcctgtg	ctgtgggccc	aagctggccg	octgtggcat	cgtoctcagc	120
gcctggggag	tgatcatgtt	gataatgctc	gggatatttt	tcaatgtcca	ttctgctgtg	180
ttaattgagg	atgtcccctt	cacagagaaa	gattttgaga	acggccctca	gaacatatac	240
aacctgtacg	agcaagtcag	ctaâaactgt	ttcatcgccg	cgggcctcta	cctcctcctc	300
gggggcttct	ccttctgcca	agttcgtctc	aataagcgca	aggaatacat	ggtgcgctag	360
agcgagtc	gactctcccc	attccctccc	ttattttaaag	actcctcagt	ccatctgttc	420
cactcatctg						430

&lt;210&gt; 402

&lt;211&gt; 190

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 402

ccgaatacgc	ggccgcgtcg	acatactgcc	tgtagagtta	gtatttctgt	tttttatatg	60
ttgcacactg	aattgaagaa	atgttgggtt	ttcttgtttt	gttttagttt	gtttctttgg	120
ttttgttttt	ggttttgctt	tttacttccc	aggtttgact	atttgccaat	gccgtcgacg	180
cgccgcgcaa						190

&lt;210&gt; 403

&lt;211&gt; 1774

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 403

ccaaagtgga	gggcgagggc	cggggcccgt	gggctctggg	gctgctgcgc	accttcgacg	60
ccggcgaaat	cgcaggctgg	gagaaggctg	gctcgggccc	cttcgggcag	gtgtacaagg	120
tgcgccatgt	gcactggaag	acgtggctcg	cgatcaagtg	ctcggccagt	ctgcacgtcg	180
acgcagggga	acgaatggag	ctcctggagg	aagctaagaa	gatggagatg	gccaagttcc	240
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<211> 372  
<212> DNA  
<213> Mouse

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caccctgact gctgacttac agctatgagg tcccggcttc tgctgcccgt gcccatttg 180  
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gcgtcccca gcctggatga ctacgtcagg tgtatctgtc agctggcaca gcccacctca 300  
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<211> 396  
<212> DNA  
<213> Mouse

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gcgggcactt tcatcgcccc tcctgtctac tccaacatca ccccttacca gagccacctg 240  
cgctctcccg tgcgccttgc tgaccacccc tctgagcggg gctttgagcc ccccccttac 300  
acaccacccc ccattctcag ccccgctccg gaaggctctg gcctctactt caatgccatc 360  
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<210> 406  
<211> 444  
<212> PRT  
<213> Rat

<400> 406  
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Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu  
35 40 45  
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr  
50 55 60  
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val  
65 70 75 80  
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile  
85 90 95  
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr  
100 105 110  
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn  
115 120 125  
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg  
130 135 140  
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu  
145 150 155 160

Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser  
 165 170 175  
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe  
 180 185 190  
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp  
 195 200 205  
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser  
 210 215 220  
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys  
 225 230 235 240  
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu  
 245 250 255  
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu  
 260 265 270  
 Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp  
 275 280 285  
 Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser  
 290 295 300  
 Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys  
 305 310 315 320  
 His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe  
 325 330 335  
 Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe  
 340 345 350  
 Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val  
 355 360 365  
 Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val  
 370 375 380  
 Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys  
 385 390 395 400  
 Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys  
 405 410 415  
 Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys  
 420 425 430  
 Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys  
 435 440

<210> 407  
 <211> 53  
 <212> PRT  
 <213> Mouse

<400> 407  
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 Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro  
 20 25 30  
 Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp  
 35 40 45  
 Glu Gly Ser Thr Met  
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<210> 408  
 <211> 119  
 <212> PRT  
 <213> Rat

<400> 408  
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 Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile  
 35 40 45  
 Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp  
 50 55 60  
 Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr  
 65 70 75 80  
 Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu  
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 Arg Lys Glu Tyr Met Val Arg  
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 <211> 590  
 <212> PRT  
 <213> Mouse

<400> 409  
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 35 40 45  
 Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg  
 50 55 60  
 Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg  
 65 70 75 80  
 Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val  
 85 90 95  
 Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu  
 100 105 110  
 Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val  
 115 120 125  
 Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp  
 130 135 140  
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile  
 145 150 155 160  
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp  
 165 170 175  
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu  
 180 185 190  
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr  
 195 200 205  
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe  
 210 215 220  
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly  
 225 230 235 240  
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys  
 245 250 255  
 Ala Ser Leu Ile Gly Ile Met Gln Arg Cys Trp His Ala Asp Pro Gln

Val	Arg	Pro	Thr	Phe	Gln	Glu	Ile	Thr	Ser	Glu	Thr	Glu	Asp	Leu	Cys
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Glu	Lys	Pro	Asp	Glu	Glu	Val	Lys	Asp	Leu	Ala	His	Glu	Pro	Gly	Glu
		290					295					300			
Lys	Ser	Ser	Leu	Glu	Ser	Lys	Ser	Glu	Ala	Arg	Pro	Glu	Ser	Ser	Arg
305					310					315					320
Leu	Lys	Arg	Ala	Ser	Ala	Pro	Pro	Phe	Asp	Asn	Asp	Cys	Ser	Leu	Ser
				325					330					335	
Glu	Leu	Leu	Ser	Gln	Leu	Asp	Ser	Gly	Ile	Ser	Gln	Thr	Leu	Glu	Gly
			340					345					350		
Pro	Glu	Glu	Leu	Ser	Arg	Ser	Ser	Ser	Glu	Cys	Lys	Leu	Pro	Ser	Ser
		355					360					365			
Ser	Ser	Gly	Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val	Asp	Ser	Ala	Phe
		370				375					380				
Ser	Ser	Arg	Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg	Glu	Ala	Ser	Thr
385					390					395					400
Gly	Asp	Leu	Gly	Pro	Thr	Asp	Ile	Gln	Lys	Lys	Lys	Leu	Val	Asp	Ala
				405					410					415	
Ile	Ile	Ser	Gly	Asp	Thr	Ser	Arg	Leu	Met	Lys	Ile	Leu	Gln	Pro	Gln
			420					425					430		
Asp	Val	Asp	Leu	Val	Leu	Asp	Ser	Ser	Ala	Ser	Leu	Leu	His	Leu	Ala
		435					440					445			
Val	Glu	Ala	Gly	Gln	Glu	Glu	Cys	Val	Lys	Trp	Leu	Leu	Leu	Asn	Asn
		450				455					460				
Ala	Asn	Pro	Asn	Leu	Thr	Asn	Arg	Lys	Gly	Ser	Thr	Pro	Leu	His	Met
465					470					475					480
Ala	Val	Glu	Arg	Lys	Gly	Arg	Gly	Ile	Val	Glu	Leu	Leu	Leu	Ala	Arg
				485					490					495	
Lys	Thr	Ser	Val	Asn	Ala	Lys	Asp	Glu	Asp	Gln	Trp	Thr	Ala	Leu	His
			500					505					510		
Phe	Ala	Ala	Gln	Asn	Gly	Asp	Glu	Ala	Ser	Thr	Arg	Leu	Leu	Leu	Glu
		515					520					525			
Lys	Asn	Ala	Ser	Val	Asn	Glu	Val	Asp	Phe	Glu	Gly	Arg	Thr	Pro	Met
		530				535					540				
His	Val	Ala	Cys	Gln	His	Gly	Gln	Glu	Asn	Ile	Val	Arg	Thr	Leu	Leu
545					550					555					560
Arg	Arg	Gly	Val	Asp	Val	Gly	Leu	Gln	Gly	Lys	Asp	Ala	Trp	Leu	Pro
				565					570					575	
Leu	His	Tyr	Ala	Ala	Trp	Gln	Gly	His	Leu	Pro	Ile	Gly	Lys		
			580					585					590		

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 <212> DNA  
 <213> Human

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ctggaagatc ataacagtta ctgcatcaac ggtgcttgtg cattccacca tgagctagag	240
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ccttacaatg tctgttctgg agaaagacga ccactgtga	339

<210> 411  
 <211> 285

<212> DNA  
<213> Human

<400> 411  
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ggacccatag ccttgaagtt ctcacacctt tgccctggaag atcataacag ttactgcatc 180  
aacggtgctt gtgcattcca ccatgagcta gagaaagcca tctgcagggtg tctaaaattg 240  
aatcgcctt acaatgtctg ttctggagaa agacgaccac tgtga 285

<210> 412  
<211> 460  
<212> DNA  
<213> Human

<400> 412  
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ctggaagatc ataacagtta ctgcatcaac ggtgcttggtg cattccacca tgagctagag 180  
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cgaccactgt gaggcctttg tgaagaattt tcatcaaggc atctgtagag atcagtgagc 300  
ccaaaattaa agttttcaga tgaacaaca aaacttgtca agctgactag actcgaaaat 360  
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<210> 413  
<211> 112  
<212> PRT  
<213> Human

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Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile  
35 40 45  
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His  
50 55 60  
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu  
65 70 75 80  
Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Leu  
85 90 95  
Lys Leu Lys Ser Pro Tyr Asn Val Cys Ser Gly Glu Arg Arg Pro Leu  
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<210> 414  
<211> 94  
<212> PRT  
<213> Human

<400> 414  
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Ala Gln Gln Ala Asp Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser



35 40 45  
 His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys  
 50 55 60  
 Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Leu Lys Leu  
 65 70 75 80  
 Lys Ser Pro Tyr Asn Val Cys Ser Gly Glu Arg Arg Pro Leu  
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<210> 415  
 <211> 73  
 <212> PRT  
 <213> Human

<400> 415  
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 Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu  
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 Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu  
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 Val Cys Ser Gly Glu Arg Arg Pro Leu  
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<210> 416  
 <211> 312  
 <212> DNA  
 <213> Human

<400> 416  
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 cgaccactgt ga 312

<210> 417  
 <211> 103  
 <212> PRT  
 <213> Human

<400> 417  
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 Ala Gln Gln Ala Asp Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser  
 35 40 45  
 His Leu Cys Leu Gly Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys  
 50 55 60  
 Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Phe Thr Gly  
 65 70 75 80  
 Tyr Thr Gly Glu Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys  
 85 90 95  
 Ser Gly Glu Arg Arg Pro Leu

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<210> 418  
 <211> 846  
 <212> DNA  
 <213> Rat

&lt;400&gt; 418

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<210> 419  
 <211> 960  
 <212> DNA  
 <213> Mouse

&lt;400&gt; 419

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<210> 420  
 <211> 1330  
 <212> DNA  
 <213> Mouse

&lt;400&gt; 420

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gtctatctca	ggctaggccc	tgagggtcta	tctcaggcta	ggccctgagg	gtctatctca	960
ggatagatgg	atttaactgc	ttttctcaag	acgcttttac	tctctcgttg	aattcttttt	1020
aaacttttaa	ttgacattgt	acttgcatc	ttatgggaaa	cagggtgacc	cacacacatg	1080
tgtacacagg	tacacacaca	gtcaggtcag	catagctggg	atgttgttgt	ttatgttggg	1140
gacagtcaga	ttggtattgt	ttttgcactg	tgctgtggaa	cattggaaaa	ccttatctga	1200
tggtgaccct	gtgcctacta	acagccctca	ctaggatata	ttttggagtc	tctggcaacc	1260
acaaattttg	tctatttcca	tgagtcagc	atctctacta	ctgcatagaa	gtaaaaaaa	1320
aaaaaaaa						1380

<210> 421  
 <211> 880  
 <212> DNA  
 <213> Mouse

<400> 421						
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tttgcttggg	ggaggggagc	agttctagtt	ccatgaggca	caaattggag	tcaaaagagca	180
acttgccgat	gtctctcttc	tcctccact	gtgtgggtag	taggaattga	atcagggttat	240
cgatcttggg	gctgagccat	ctctgtggcc	cacagagcac	ttatatgttg	ttacttgttg	300
ctctcacatt	gtcagtgtac	agcttgggtg	cctttgtcac	tgccatgtct	tgtagactg	360
ttgtgataaa	aatgtttgat	agtttacaca	aatctagtaa	attgaaccca	agagccaagt	420
gtgggtgggt	acccttaatt	ccagcacttt	gggggcaagt	tcaggtagtt	ctctgaattt	480
gagagcctcc	tggccacat	agttagttcc	atggctgctg	agttgcaaaa	gaacaccaac	540
acctttcccc	cacaaataga	attgtactga	aggtcacagt	cagagaaaag	atagcaagga	600
tggctgtctc	gagccctccc	tgtgcacttc	tgtagacctc	gccccgggtg	ctaaatggag	660
tctgatttta	gcacctgcac	ttgactgctg	tgctccacc	tgacccgct	tytctgctg	720
ccagattgct	agaactttga	ccaaaatggg	acttaattgg	agttgtgatt	ggkatgttca	780
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aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa			880

<210> 422  
 <211> 533  
 <212> DNA  
 <213> Mouse

<400> 422						
cctaaatgct	gggattaaag	gcgtgcgcca	ctactgccag	gctgtttttt	ttttttttt	60
ttttttatta	atgatctgcc	agacaaagag	atgtcctttt	tggtgcaaaa	gtcaccat	120
gcttgaagtc	actatatttg	attagctctg	taactgatac	acaaataaaa	ctttccatta	180
tggataatac	attatctatt	attattttat	tcttgttcat	ttttgcaatt	tctgtacttg	240
actccagtt	gagtacaagg	tgcttttggg	ggtttttcaa	ggatcttgag	gttacatgaa	300
attgctgatg	atgtctgttg	aaagcattgt	atggaggcct	gaggtatatt	tggcctgaga	360
gcagagtttt	taaaaatagag	cctgctggaa	aagctagctg	gagcttctga	ctactttaga	420
aaggcactgt	ttgaagcaca	ggccatgaag	taagacttgc	tttctagtta	aattgaggtt	480
ttttgttttt	ttaagtcowt	agtgtataga	gatttccctac	attttttgtg	gtt	533

<210> 423  
 <211> 738  
 <212> DNA  
 <213> Rat

<400> 423

ataaggcaca	tttgcttcat	aaaataaaaa	aaaaggaaat	ttacttagcc	gcattgtcagt	60
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attctaggga	ataaacatgc	aaatcagatg	gagctcaatc	tgacggcgct	gacacctctcc	180
ccctgggttg	cagtctgtgc	acctcctgga	ttcgcccgcg	accaggcagt	cagaggcctg	240
gctcttgacg	gcaggaggat	cactgttgta	aagaacagcg	tcacatttag	cgcatctggc	300
gtagtagcag	tttttaacac	tttgcgcagg	tgccctccct	ccccacccg	cgctttgtta	360
ggtctacctc	tctaaatctc	tgccctcctc	gcacagtaag	tgacctctcc	atgacaaaagg	420
gccccagac	agcagttata	aatcaatgtg	ttttgggttt	gtttgtttgt	ttgttttgtt	480
ttaaagaaaa	acccggccat	gcttgggtggc	acttgccctt	aatagtagcg	cttggtagac	540
agaggcaagc	ggttctctgt	aagtccaagg	ccagcctggg	ctacacagtg	agaccgggtc	600
tcaaaaacaa	aacaacaaaa	aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	660
gatcactgtc	tgcaaaactaa	agtgacttga	gctcctgtca	cagcctttcc	agcaagggca	720
agcttcttta	ttagtatt					738

<210> 424  
 <211> 1035  
 <212> DNA  
 <213> Rat

<400> 424

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cctgttggtc	ttgcttttcc	tcccattttg	cctgtgtcaa	gatgaataca	tggagctctc	180
acaagctgga	ggactgcccc	cagactgcag	caagtgttgc	catggagatt	atggattccg	240
tggttaccaa	gggccccctg	gacccccagg	tctcctctgc	attccaggaa	accatggaaa	300
caatggaaat	aacgggagcca	ctggccacga	agggggccaag	ggtgagaaaag	gagacaaaagg	360
cgacctgggg	cctcgagggg	aacgggggca	gcattggccc	aaaggataga	agggatcccc	420
aggggtgcca	ccagagctgc	agattgcgtt	catggcttct	ctagcgactc	acttcagcaa	480
tcagaacagt	ggcattatct	tcagcagttg	tgagaccaac	attggaaact	tcttcgatgt	540
catgactggg	agatttgggg	cccccgatc	aggcgtgtat	ttcttcacct	tcagcatgat	600
gaagcatgag	gacgtggagg	aagtgtatgt	gtaccttatg	cacaatggta	acacggtgtt	660
cagcatgtac	agctatgaaa	caaagggaaa	atcagataca	tccagcaacc	atgcagtgtc	720
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tcaggatagc	tccatgctaa	gggcgatttg	taggtgagct	agggttggtta	ggatctgagg	900
ggtgttgagg	ttgggcttct	ctatggagta	tttaactgtt	acattggtca	cactgtctact	960
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ggtaatatcc	ccaga					1035

<210> 425  
 <211> 835  
 <212> DNA  
 <213> Rat

<400> 425

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cttactatc	ctggccctgg	gtgctgtggg	ctgtggccca	gcgggactct	ggtgatgcca	180
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tcagcttgct	gctgcaagcc	cttctcctgc	tgctcgtct	accacatgca	ccgggcagcg	360
agggggtgag	ctcccgtcc	gctcggatth	cttcggacct	tctcaggaac	atagtgcccta	420
ccagacaatt	gactcgtcag	actcacctgc	agacccccctt	gcaagcctgg	agaacaaggg	480
ccaagctgcc	ccccgggggt	actgaagctg	tcctgggccc	tcctggggcc	cagcaggatg	540
cttggtcacct	tctttactgg	acctacaatg	gggtatccctc	cattccctgc	cacagagggtg	600
gcctgagtc	tgtgcccctg	gaggtcccag	ctgagaagag	cccagtccta	attctccatg	660
ctgcccctcc	attcaagaca	cctgttaacc	cctgggctag	aactgtgggt	ggtttcttcc	720
cctcctcccc	atcactataa	cacacaaccg	ccgagctgtg	cagagtgttc	agggccatcc	780
aggccttatg	ggccaatgat	cactgcctct	caggctaccc	caaggtgacc	cagcc	835

&lt;210&gt; 426

&lt;211&gt; 1337

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (626) ... (626)

&lt;400&gt; 426

accggcctca	ctatgtctgc	cattttcaat	tttcagagtc	tgttgactgt	aatcttgctg	60
cttatatgta	catgtgctta	tatccgatcc	ctggcaccca	gcacccctga	cagaaataaa	120
actggactat	tggaatatt	ttggaagtgt	gcccgaaattg	gggaacgcaa	gagtccttat	180
gtogccatat	gctgtatagt	gatggccttc	agcatcctct	tcatacagta	gctttggaaa	240
ctaccagcat	gtgcttgcta	tcagactgta	aacaaggact	tgccctccaga	aaataatggg	300
aagaattggt	aagccatttg	tctctgaaca	tggaatgaga	taaacttcaa	gatgctgttc	360
tctattttta	tgctattgga	ccaatgagct	gaatgaataa	ttaagatgta	acagttcaat	420
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tcagggttcag	ctgaaaatca	gttactgttt	caaaacaaag	aggaattaaa	tcctagctga	1260
aaactataca	tagcatttat	taattaatca	ctgggtttta	ctgctctttt	taaaagtttg	1320
aaaaaaaaaa	aaaaaaaa					1337

&lt;210&gt; 427

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 427

gctagtcgaa	tgtccgggct	goggacgctg	ctggggctgg	ggctgctgg	tgccgggctcg	60
cgccctgccac	gggtcatcag	ccagcagagt	gtgtgtcgtg	caaggcccat	ctggtgggga	120
acacagcgcc	ggggctcgga	gaccatggcg	ggcgctgcgg	tgaagtactt	aagtcaggag	180
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atgtccaaga	gtccccgcac	tgtcttggtc	atctgtggcc	ccggaaataa	cggaggggat	360
gggdtgggtc	gtgcgcgaca	cctcaaactt	tttgggttacc	agccaactat	ctattacccc	420

aaaagaccta	acaagcccct	cttcactggg	ctagtgactc	agtgtcagaa	aatggacatt	480
ccttttccttg	gtgaaatgcc	cccagaggat	gggatgtaga	gaagggaaac	cctagcggaa	540
tccaaccaga	cttactcatt	tcactgacgg	cacccaagaa	gtctgcaact	cactttactg	600
gccgatataca	ttaccttggg	ggctgccttg	taccacctgc	tctagagaag	aagtaccagc	660
tgaacctgcc	atcttaccct	gacacagagt	gtgtctaccg	tctaagataa	gggaggtggg	720
taggcaggat	tctcaataaa	gacttgggtac	tttctgtctt	gaaaaaaaaa	aaaaaaaaaa	780

<210> 428  
 <211> 460  
 <212> DNA  
 <213> Mouse

<400> 428						
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cgctgccttt	tcagctgcgc	agcatcgttc	ttatatgcga	ctaacagaaa	aggagatga	120
atcattacca	atagatatag	ttcttcagac	acttctggcc	tttgcagtta	cctgttatgg	180
catagttcat	atcgaggggg	agttcaaaga	catggatgcc	acttcagaat	taaagaataa	240
gacatttgat	accttaagga	atcaccatc	tttttatgtg	tttaaccatc	gtggctcgagt	300
gctgttcctgg	ccttcagatg	caacaaattc	ttcaaaccta	gatgcattgt	cctctaatac	360
atcgttgaag	ttacgaaagt	ttgactcact	gcgcctgtaa	gctttttaca	aattaaataa	420
caggacagac	acagaattga	gtattggagt	ttgggtgtga			460

<210> 429  
 <211> 472  
 <212> DNA  
 <213> Mouse

<400> 429						
gaagcctctt	cccatggaag	cacactctag	gagagagaag	gcctctgggc	tccgcctggc	60
ctggcattat	gaatgcagtg	gggtcagtg	gtgggtggatg	tgtgtactgg	gttggctttc	120
cttttttagtt	tttttacttt	ttagtttagt	ttgttctttt	ccttcccaa	taaatcattc	180
tcacatgctt	ccatgtttgt	ttctgagagg	tgggggtcca	aatgtataga	aagtaggccc	240
cagtccataa	ggagggtgtga	acacaccccc	ttactgctta	tcacccattt	gacaggaacg	300
ccaggagggg	gagggggagg	ggaagaggtg	agttctgcac	agtcggacat	ttctgttgct	360
tttgcattgt	taatatagac	gttcctgtcg	atccttggga	gatcatggcc	ttcagatatg	420
cacacgacct	ttgaattgtg	cctactaatt	atagcagggg	acttgggtac	cc	472

<210> 430  
 <211> 954  
 <212> DNA  
 <213> Mouse

<400> 430						
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ccacagaaat	cctttattca	catgttggtta	aacctgtccc	ggcacacccc	agcagcaaca	180
gcaccttgaa	tcaagccagg	aatggaggca	ggcatttcag	tagcactgga	ctggatcgaa	240
acagtgcagt	tcaagtgggc	tgcagggaac	tgcggtccac	caaatacatt	tcggacggcc	300
agtgcaccag	catcagccct	ctgaaggagc	tgggtgtgag	gggagagtgc	ttgcccctgc	360
cggtgcttcc	caactggatc	ggaggaggct	acggaacaaa	gtactggagc	cggaggagct	420
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gtttgcagtg	aaagccaggc	atcctgtagt	ttccatcccc	cccccatcc	cagtcatttc	900
tttaaaagca	cctgatgctg	cattctgtta	cagtttaaaa	aaaaaaaaa	aaaa	954

<210> 431  
 <211> 780  
 <212> DNA  
 <213> Mouse

<400> 431						
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cgccctgcac	gggtcatcag	ccagcagagt	gtgtgtcgtg	caaggcccat	ctgggtgggga	120
acacagcgcc	ggggctcggg	gaccatggcg	ggcgtgcggg	tgaagtactt	aagtcaggag	180
gaggctcagg	ccgtggacca	agagcttttt	aacgagtatc	agttcagcgt	ggatcaactc	240
atggagctgg	ccgggttgag	ctgtgccacg	gctattgcca	aggcttatcc	ccccacgtct	300
atgtccaaga	gtccccgcac	tgtcttggtc	atctgtggcc	ccggaataa	cggaggggat	360
gggctggtct	gtgcgcgaca	cctcaaaact	tttggttacc	agccaactat	ctattacccc	420
aaaagacctt	acaagccctt	cttcaactgg	ctagtgcact	agtgtcagaa	aatggacatt	480
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tccaaccaga	cttactcatc	tcaactgacg	caccaagaa	gtctgcaact	cactttactg	600
gccgatatca	ttaccttggg	ggtcgctttg	taccacctgc	tctagagaag	aagtaccagc	660
tgaacctgcc	atcttacctt	gacacagagt	gtgtctaccg	tctacagtaa	gggagggtgg	720
taggcaggat	tctcaataaa	gacttggtac	tttctgtctt	gaaaaaaaa	aaaaaaaaa	780

<210> 432  
 <211> 1144  
 <212> DNA  
 <213> Mouse

<400> 432						
cttctcaggg	cctgccaccc	aaataagtct	ggccctagcc	tcaactctct	ctcaggctgg	60
gccacaggaa	gctgctgact	ggccacttga	caccctcccc	ctaaagctaa	tgtctgtgac	120
tataggagg	ttagcacttt	ttctaattgg	aattctttct	tgtcctgtgg	ccccatccct	180
caccgcctct	tggcctggac	cagatacatg	cagcctcttt	ctccagcaca	gcctttccct	240
gagcctgagg	ttagggcaga	gttttagaggg	tgggctaaagt	gtatgttttc	atgtatgcat	300
tcatgcctgt	gagtgtgtgg	cttgctgtcg	tgtcctctgg	gatcccaagc	cacgcgggtc	360
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caaaaaatac	tctgaagggc	gggaggatac	ccaagcctga	tgccctgagag	gagtccttag	660
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tcctggcatt	gggctccggc	tctacctccc	caagcagggc	gaggccccgc	cttctcagcc	1020
tagcaccacc	tgtccccgag	tcttctcagc	ttgcccacac	ttctcggcgc	ccacacaggt	1080
gacagtccca	agtagataac	ctccatggga	caagttgggt	gttgccctta	ccgcctgccc	1140
agcc						1144

<210> 433  
 <211> 438  
 <212> DNA  
 <213> Mouse

<400> 433						
cttgagtctg	gagtgtctga	aataatagta	tgcactatcc	ctgcctggca	tgttttgtttg	60

ttaatgtgca	ctggtgtttt	gcctggatgt	gtatacttgt	gaagatgtca	gaactcctgg	120
agctggagtt	agagacaatg	gtgagctgcc	ttgtggatgt	tgggaattga	acccagggtcc	180
tctggagaaa	taaccagtgc	tcttaaccac	taagccatct	caacagcccc	aaattatttt	240
tttaataagt	tgcctcggtc	atgttgtctt	aatcagagcg	atagaaaagt	aactaatata	300
gattatttat	gaattcaggt	ggcttaatgg	tatatgcatg	aattagtagt	aaaacaagaa	360
ctagggccag	caagtggctt	aagggtgcct	gctaaccatc	tcagccacct	gagttcagtc	420
tccaggaacc	acacagtg					438

<210> 434  
 <211> 383  
 <212> DNA  
 <213> Mouse

<400> 434						
cccacgtcta	tgttcacctt	cgttgtttctg	gtaatcacca	tcgtcatctg	tctctgccac	60
gtctgctttg	gacacttcaa	atacctcagt	gcccacaact	acaagattga	acacacagag	120
acagatgccg	tgagctccag	aagtaatgga	cggcccccca	ctgctggcgc	tgccccaaa	180
tctgcgaaat	acatcgctca	ggtgctgcag	gactcagagg	gggacgggga	cggagatggg	240
gctcctggga	gctcaggcga	tgagccccca	tcgtcctcct	ccaagacga	ggagttgctg	300
atgcctcctg	atggcctcac	ggacacagac	ttccagtcac	gcgaggacag	cctcatagag	360
aatgagattc	accagtaagg	ggt				383

<210> 435  
 <211> 405  
 <212> DNA  
 <213> Rat

<220>  
 <221> unsure  
 <222> (114) ... (114)

<221> unsure  
 <222> (346) ... (346)

<221> unsure  
 <222> (353) ... (353)

<221> unsure  
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 <213> Rat

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 <213> Mouse

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&lt;211&gt; 2401

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 439

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 <221> unsure  
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 <211> 1744  
 <212> DNA  
 <213> Rat

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&lt;210&gt; 444

&lt;211&gt; 2157

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 444

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&lt;210&gt; 445

&lt;211&gt; 2250

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (2219) ... (2219)

&lt;400&gt; 445

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&lt;210&gt; 446

&lt;211&gt; 1685

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1482) ... (1482)

&lt;400&gt; 446

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&lt;210&gt; 447

&lt;211&gt; 1890

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 447

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 <212> DNA  
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<400> 448

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<400> 450						
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<210> 451  
 <211> 1225  
 <212> DNA  
 <213> Mouse

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 <211> 445  
 <212> DNA  
 <213> Mouse

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<210> 453  
 <211> 2792  
 <212> DNA  
 <213> Mouse

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<210> 454  
 <211> 1808  
 <212> DNA  
 <213> Mouse

<400> 454

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&lt;210&gt; 455

&lt;211&gt; 1121

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1095)...(1095)

&lt;400&gt; 455

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&lt;210&gt; 456

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 456

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Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys Ala Ser Gly
1          5          10          15
Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser Val Trp Trp
20          25          30
Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu Leu Phe Ser
35          40          45
Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His Met Leu Pro
50          55          60
Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
65          70          75

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&lt;210&gt; 457

&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; Rat

<400> 457  
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 Leu Lys Lys Cys Trp Phe Phe Leu Phe Cys Phe Ser Leu Phe Leu Trp  
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 Phe Cys Phe Trp Phe Cys Phe Leu Leu Pro Arg Phe Asp Tyr Leu Pro  
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 Met

<210> 458  
 <211> 296  
 <212> PRT  
 <213> Mouse

<400> 458  
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 Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr Cys Ile Cys  
 35 40 45  
 Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys Pro Gln Asp  
 50 55 60  
 Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg Asn Gly Gly  
 65 70 75 80  
 Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met  
 85 90 95  
 Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala  
 100 105 110  
 Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr  
 115 120 125  
 Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu  
 130 135 140  
 Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln Arg Val Cys  
 145 150 155 160  
 Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Arg Cys Leu  
 165 170 175  
 Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly Cys Lys Pro  
 180 185 190  
 Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys Pro Thr Gly  
 195 200 205  
 Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg  
 210 215 220  
 Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro  
 225 230 235 240  
 Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Ala Asp Cys Asp Pro  
 245 250 255  
 Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly Pro Thr Cys  
 260 265 270  
 Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala Pro Gln His  
 275 280 285  
 Ser Ser Ser Lys Ala Met Lys His  
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<210> 459

<211> 106  
 <212> PRT  
 <213> Mouse

<400> 459  
 Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly  
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 Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu  
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 Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Tyr  
 35 40 45  
 Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Ser  
 50 55 60  
 Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile Cys Ile Asn  
 65 70 75 80  
 Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr Asp Val Ala  
 85 90 95  
 Lys Arg Met His Ala Cys Thr Ala Ser Thr  
 100 105

<210> 460  
 <211> 53  
 <212> PRT  
 <213> Mouse

<400> 460  
 Met Cys Ala Gly His Gly Gln Ser Leu Leu Ile Ala Ser Asp Asp Gly  
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 Arg Val Ser Arg Gln Pro Trp Ser Cys Leu Asn Ile Val Ser Asn Cys  
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 His Ser Phe Arg Glu Arg Gly Thr Ser Ser Pro Leu Leu Leu Ala Leu  
 35 40 45  
 Pro Asp Arg Pro Leu  
 50

<210> 461  
 <211> 261  
 <212> PRT  
 <213> Mouse

<400> 461  
 Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile Val Phe Ala  
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 Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile Ser Trp Ser  
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 Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro His His His  
 35 40 45  
 His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu Leu Thr His  
 50 55 60  
 Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val Leu Trp Leu  
 65 70 75 80  
 Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg Lys Phe Val  
 85 90 95  
 His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala Cys Ile Val  
 100 105 110  
 Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe Gly Lys Arg  
 115 120 125

Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala Thr Lys Ser  
 130 135 140  
 Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met Gln Asp Leu  
 145 150 155 160  
 Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp Pro Leu Tyr  
 165 170 175  
 Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly Tyr Arg Pro  
 180 185 190  
 Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp Ser Asp Asn  
 195 200 205  
 Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys Pro Leu Gly  
 210 215 220  
 Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu Thr Arg Glu  
 225 230 235 240  
 Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys Ala Met Pro  
 245 250 255  
 Ser Asp Met Asp Ser  
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<210> 462  
 <211> 138  
 <212> PRT  
 <213> Mouse

<400> 462  
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 20 25 30  
 Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln Tyr Glu Asp  
 35 40 45  
 Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln Val Thr Thr  
 50 55 60  
 Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile Phe Thr Leu  
 65 70 75 80  
 Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg Val Arg Leu  
 85 90 95  
 Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu Arg Ser Glu  
 100 105 110  
 Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe Gly Ser Leu  
 115 120 125  
 Thr Gly Gly Ile Leu Ser Thr His Ser Pro  
 130 135

<210> 463  
 <211> 314  
 <212> PRT  
 <213> Mouse

<400> 463  
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 Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met  
 20 25 30  
 Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile  
 35 40 45  
 Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr

50	55	60
Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly		
65	70	75
Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His		80
	85	90
Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys		95
	100	105
Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln		110
	115	120
Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser		125
	130	135
Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr		140
	145	150
Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu		155
	160	165
Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly		170
	175	180
Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu		185
	190	195
Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly		200
	205	210
Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg		215
	220	225
Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala		230
	235	240
Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly		245
	250	255
Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln		260
	265	270
Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe		275
	280	285
Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys		290
	295	300
305	310	

<210> 464  
 <211> 1663  
 <212> DNA  
 <213> Mouse

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 <212> PRT  
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Lys	Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro
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Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Val	Thr	Thr	Lys	Ser
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&lt;400&gt; 467

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&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 468

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&lt;211&gt; 1500

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 469

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&lt;211&gt; 2795

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 475

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&lt;211&gt; 1953

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 476

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&lt;212&gt; DNA

&lt;213&gt; Rat

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 <213> Rat

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&lt;210&gt; 482

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 482

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 <212> DNA  
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 <211> 1274  
 <212> DNA  
 <213> Mouse

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 <211> 858  
 <212> DNA  
 <213> Human

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<210> 487  
 <211> 2128  
 <212> DNA  
 <213> Mouse

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<210> 488  
 <211> 95  
 <212> PRT  
 <213> Rat

<400> 488  
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      20           25           30
Glu Gly Leu Cys Arg Leu Trp Thr Ala Thr Cys His Ser Arg Gly Glu
      35           40           45
Ser Glu Val Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln
      50           55           60
Gly Ser Leu Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys
      65           70           75           80
Ala His Thr Ser Met Asp Arg Thr Leu Gly Leu Leu Ser Cys Cys
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<210> 489
<211> 207
<212> PRT
<213> Human

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      <400> 489
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Leu Pro Met Ser Leu Ala Phe Leu Phe Leu Phe Pro Ser Ala Ile
      20           25           30
Leu Thr Leu Ile Val Cys His Ile Asn Ser Pro Gly Cys Val Phe Phe
      35           40           45
Ser Arg Lys Lys Leu Lys Gly Lys Thr Lys Pro Lys Lys Pro Glu Thr
      50           55           60
Thr Asn Lys Asn Gly Asn Asp Asn Gly Cys Leu Ser Phe Phe Cys His
      65           70           75           80
Asp Phe Pro Asp Leu Val Cys Ser Leu Cys Leu Arg Glu Ala Gly Asp
      85           90           95
Val Asp Glu Ala Val Phe Phe Phe Leu Phe Leu Val Phe Glu Thr Arg
      100          105          110
Val Ser Leu Cys His Pro Gly Trp Ser Val Thr Trp His Asp Leu Ser
      115          120          125
Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Arg Leu Ser Cys Leu Ser
      130          135          140
Leu Leu Ser Ser Trp Asp Tyr Arg His Ala Pro Leu Cys Pro Asp Asn
      145          150          155          160
Phe Phe Val Phe Leu Val Glu Thr Gly Phe His His Val Gly Gln Ala
      165          170          175
Gly Leu Glu Leu Leu Thr Ser Gly Tyr Pro Pro Thr Leu Ala Ser Gln
      180          185          190
Ser Ala Gly Ile Ile Gly Met Asn His Arg Ala Trp Pro Lys Met
      195          200          205

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<210> 490
<211> 81
<212> PRT
<213> Human

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      <400> 490
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Gly Ile Ile Gly Met Ser His Cys Ile Lys Pro Val Lys Ser Ile Tyr
      20           25           30
Ile Lys Leu Asp Cys Arg Lys Arg Asp Lys Thr Ser Leu Leu Phe
      35           40           45

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Cys Pro Gln Gly Pro Arg Asn Pro Val Ser Lys Ala Pro His Gln Leu  
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 Gln Cys Val Pro Val Ser Arg Val Pro Thr Gly Thr Glu Ser Ser Gly  
 65 70 75 80  
 Thr

<210> 491  
 <211> 193  
 <212> PRT  
 <213> Human

<400> 491  
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 1 5 10 15  
 Ile Arg Ser Trp Leu Thr Arg Lys His Ile Gln Arg Leu His Ala Ala  
 20 25 30  
 Ala Thr Val Ile Lys Arg Ala Trp Gln Lys Trp Arg Ile Arg Met Ala  
 35 40 45  
 Cys Leu Ala Ala Lys Glu Leu Asp Gly Val Glu Glu Lys His Phe Ser  
 50 55 60  
 Gln Ala Pro Cys Ser Leu Ser Thr Ser Pro Leu Gln Thr Arg Leu Leu  
 65 70 75 80  
 Glu Ala Ile Ile Arg Leu Trp Pro Leu Gly Leu Val Leu Ala Asn Thr  
 85 90 95  
 Ala Met Gly Val Gly Ser Phe Gln Arg Lys Leu Val Val Trp Ala Cys  
 100 105 110  
 Leu Gln Leu Pro Arg Gly Ser Pro Ser Ser Tyr Thr Val Gln Thr Ala  
 115 120 125  
 Gln Asp Gln Ala Gly Val Thr Ser Ile Arg Ala Leu Pro Gln Gly Ser  
 130 135 140  
 Ile Lys Phe His Cys Arg Lys Ser Pro Leu Arg Tyr Ala Asp Ile Cys  
 145 150 155 160  
 Pro Glu Pro Ser Pro Tyr Ser Ile Thr Gly Phe Asn Gln Ile Leu Leu  
 165 170 175  
 Glu Arg His Arg Leu Ile His Val Thr Ser Ser Ala Phe Thr Gly Leu  
 180 185 190  
 Gly

<210> 492  
 <211> 104  
 <212> PRT  
 <213> Human

<400> 492  
 Met Pro Pro Asn Pro His Leu Thr Leu Ile Leu Ile Thr Ala Leu Trp  
 1 5 10 15  
 Glu Ala Val Val Gly Gly Ser Leu Lys Pro Arg Arg Leu Arg Leu Glu  
 20 25 30  
 Cys Cys Thr Ile Ala Pro Leu His Ser Thr Ala Trp Ala Thr Glu Gly  
 35 40 45  
 Asp Pro Val Ser Lys Lys Arg Glu Thr Ala Val Ala Ile Ile Val Val  
 50 55 60  
 Arg Asn Asn Thr Glu Arg Ser Leu Val Leu Ser Ala Gln Leu Phe Leu  
 65 70 75 80  
 Thr Val Ser Leu Cys Arg Thr Pro Gln Ser His Thr Arg Thr Trp Thr

85 90 95  
 Leu Met Pro Ser Gly Gly Leu Thr  
 100  
 <210> 493  
 <211> 254  
 <212> PRT  
 <213> Human  
 <400> 493  
 Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly Ala Ala His  
 1 5 10 15  
 Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro Leu  
 20 25 30  
 Pro Thr Pro Gly Pro Asp Arg Asp Glu Leu Thr Ala Asp Ser Asp  
 35 40 45  
 Val Asp Glu Phe Leu Asp Lys Phe Leu Ser Ala Gly Val Lys Gln Ser  
 50 55 60  
 Asp Leu Pro Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Ser Met  
 65 70 75 80  
 Glu Glu Ser Val Arg Gly Tyr Asp Trp Ser Pro Arg Asp Ala Arg Arg  
 85 90 95  
 Ser Pro Asp Gln Gly Arg Gln Gln Ala Glu Arg Arg Ser Val Leu Arg  
 100 105 110  
 Gly Phe Cys Ala Asn Ser Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala  
 115 120 125  
 Phe Asp Asp Ile Pro Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp  
 130 135 140  
 Arg His Gly Ala Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn  
 145 150 155 160  
 Trp Lys Arg Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly  
 165 170 175  
 Ala Pro Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn  
 180 185 190  
 Ala Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
 195 200 205  
 Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys Phe  
 210 215 220  
 Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe Arg Ser  
 225 230 235 240  
 Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe Ala  
 245 250  
 <210> 494  
 <211> 215  
 <212> PRT  
 <213> Rat  
 <400> 494  
 Met Arg Pro Val Val Pro Ile His Val Phe Ser Ser Glu Asp Ser Pro  
 1 5 10 15  
 Pro Arg Asp Ala Pro Ser Thr Ser Ser Val Ala Pro Ala Ser Arg Ala  
 20 25 30  
 Val His Thr Pro Pro Leu Gly Pro Ile Leu Lys Lys Thr Ala Gly Leu  
 35 40 45  
 Gly Phe Cys Ala Val Phe Leu Tyr Phe Ile Thr Ala Leu Ile Phe Pro  
 50 55 60



Ala Ile Ser Thr Asn Ile Gln Pro Met His Lys Gly Thr Gly Ser Pro  
65 70 75 80  
Trp Thr Ser Lys Phe Tyr Val Pro Leu Thr Val Phe Leu Leu Phe Asn  
85 90 95  
Phe Ala Asp Leu Cys Gly Arg Gln Val Thr Ala Trp Ile Gln Val Pro  
100 105 110  
Gly Pro Arg Ser Lys Leu Leu Pro Ile Leu Ala Val Ser Arg Val Cys  
115 120 125  
Leu Val Pro Leu Phe Leu Leu Cys Asn Tyr Gln Pro Arg Ser His Leu  
130 135 140  
Thr Leu Val Leu Phe Gln Ser Asp Ile Tyr Pro Ile Leu Phe Thr Cys  
145 150 155 160  
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Val Leu Met Tyr  
165 170 175  
Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Ser Val Val  
180 185 190  
Met Leu Phe Tyr Met Ser Leu Gly Leu Met Leu Gly Ser Ala Cys Ala  
195 200 205  
Ala Leu Leu Glu His Phe Ile  
210 215

<210> 495  
<211> 91  
<212> PRT  
<213> Human

<400> 495  
Met Ile Gln Pro Ser Leu Ser Val Leu Cys Gly Leu Gly Cys Ala Phe  
1 5 10 15  
Leu Trp Ala Thr Ser Ser Phe Ala Ala Val Ser Pro Pro Ala Cys Ala  
20 25 30  
Pro Ala Thr Ser Pro Ser Pro Val Val His Leu Arg Ser Thr Gln Pro  
35 40 45  
Gly Gln Ser Cys Phe Val Leu Leu His Arg Leu Gly Leu Pro Cys Val  
50 55 60  
Leu Ser Ser Ser Gly Ser Phe Ser Ser Pro His Leu Phe Cys Phe Leu  
65 70 75 80  
Pro Val Leu Val Ser Pro Cys Ala Leu Gly Pro  
85 90

<210> 496  
<211> 224  
<212> PRT  
<213> Human

<400> 496  
Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu  
1 5 10 15  
Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn  
20 25 30  
Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His  
35 40 45  
Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu  
50 55 60  
Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val  
65 70 75 80  
Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85										90					95				
Cys	Lys	Thr	Asp	Leu	Asp	Ile	Ala	Tyr	Lys	Phe	Gly	Lys	Thr	Val	Val				
100										105					110				
Ser	Cys	Glu	Gly	Tyr	Glu	Ser	Ser	Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly				
115										120					125				
Ser	Cys	Gly	Leu	Glu	Tyr	Asn	Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln				
130										135					140				
Lys	Leu	Lys	Glu	Ser	Gly	Lys	Gln	His	Gly	Phe	Ala	Ser	Phe	Ser	Asp				
145										150					155				
Tyr	Tyr	Tyr	Lys	Trp	Ser	Ser	Ala	Asp	Ser	Cys	Asn	Met	Ser	Gly	Leu				
165										170					175				
Ile	Thr	Ile	Val	Val	Leu	Leu	Gly	Ile	Ala	Phe	Val	Val	Tyr	Lys	Leu				
180										185					190				
Phe	Leu	Ser	Asp	Gly	Gln	Tyr	Ser	Pro	Pro	Pro	Tyr	Ser	Glu	Tyr	Pro				
195										200					205				
Pro	Phe	Ser	His	Arg	Tyr	Gln	Arg	Phe	Thr	Asn	Ser	Ala	Gly	Pro	Pro				
210										215					220				

<210>	497
<211>	766
<212>	PRT
<213>	Rat

<400> 497

Met 1	Leu	Leu	Leu	Leu 5	Leu	Leu	Leu	Leu	Leu 10	Pro	Ala	Cys	Pro	Leu 15	Leu	Ser
Ala	Arg	Met	Phe 20	Pro	Gly	Asn	Ala	Gly 25	Gly	Glu	Leu	Val	Thr 30	Pro	His	
Trp	Val 35	Leu	Asp	Gly	Lys	Thr	Trp 40	Leu	Lys	Val	Thr	Leu 45	Lys	Glu	Gln	
Ile 50	Ser	Lys	Pro	Asp	Ser	Gly 55	Leu	Val	Ala	Leu 60	Lys	Ala	Glu	Gly	Gln	
Asp 65	Leu	Leu	Leu	Glu 70	Leu	Glu	Lys	Asn	His	Arg 75	Leu	Leu	Ala	Pro	Gly 80	
Tyr	Thr	Glu	Thr 85	Tyr	Tyr	Ser	Arg	Asp 90	Gly	Gln	Pro	Ile	Val 95	Leu	Ser	
Pro	Asn	His	Thr 100	Asp	His	Cys	His	Tyr 105	Gln	Gly	Cys	Val	Arg 110	Gly	Phe	
Arg	Glu 115	Ser	Trp	Val	Val	Leu	Ser 120	Thr	Cys	Ser	Gly	Met 125	Ser	Gly	Leu	
Ile 130	Val	Leu	Ser	Ser	Lys	Val 135	Ser	Tyr	Tyr	Leu 140	His	Pro	Trp	Met	Pro	
Gly 145	Asp	Thr	Lys	Asp 150	Phe	Pro	Thr	His	Lys	Ile 155	Phe	Arg	Val	Glu	Gln 160	
Leu	Phe	Thr	Trp 165	Arg	Gly	Ala	Arg	Lys	Asp 170	Lys	Asn	Ser	Gln	Phe	Lys 175	
Ala	Gly 180	Met	Ala	Arg	Leu	Pro	His	Val 185	Pro	His	Arg	Arg 190	Met	Arg	Arg	
Glu	Ala 195	Arg	Arg	Ser	Pro	Lys	Tyr 200	Leu	Glu	Leu	Tyr 205	Ile	Val	Ala	Asp	
His 210	Ala	Leu	Phe	Leu	Leu	Gln 215	Arg	Gln	Asn	Leu 220	Asn	His	Thr	Arg	Gln	
Arg 225	Leu	Leu	Glu	Ile 230	Ala	Asn	Cys	Val	Asp	Gln 235	Ile	Leu	Arg	Thr	Leu 240	
Asp	Ile	Gln	Leu 245	Val	Leu	Thr	Gly	Leu 250	Glu	Val	Trp	Thr	Glu 255	Gln	Asp	
His	Ser	Arg	Ile	Thr	Gln	Asp	Ala	Asn	Glu	Thr	Leu	Trp	Ala	Phe	Leu	

				260						265				270					
Gln	Trp	Arg	Arg	Gly	Leu	Trp	Val	Arg	Arg	Pro	His	Asp	Ser	Thr	Gln				
		275					280					285							
Leu	Leu	Thr	Gly	Arg	Thr	Phe	Gln	Gly	Thr	Thr	Val	Gly	Leu	Ala	Pro				
	290					295					300								
Val	Glu	Gly	Met	Cys	His	Ala	Glu	Ser	Ser	Gly	Gly	Val	Ser	Thr	Asp				
305					310					315					320				
His	Ser	Glu	Leu	Pro	Ile	Gly	Thr	Ala	Ala	Thr	Met	Ala	His	Glu	Ile				
				325				330						335					
Gly	His	Ser	Leu	Gly	Leu	His	His	Asp	Pro	Glu	Gly	Cys	Cys	Met	Glu				
			340					345					350						
Ala	Asp	Ala	Glu	Gln	Gly	Gly	Cys	Val	Met	Glu	Ala	Ala	Thr	Gly	His				
		355					360					365							
Pro	Phe	Pro	Arg	Val	Phe	Ser	Ala	Cys	Ser	Arg	Arg	Gln	Leu	Arg	Thr				
	370					375					380								
Phe	Phe	Arg	Lys	Gly	Gly	Gly	Ala	Cys	Leu	Ser	Asn	Val	Ser	Ala	Pro				
385					390					395					400				
Gly	Leu	Leu	Val	Leu	Pro	Ser	Arg	Cys	Gly	Asn	Gly	Phe	Val	Glu	Ala				
				405					410					415					
Glu	Glu	Glu	Cys	Asp	Cys	Gly	Ser	Gly	Gln	Lys	Arg	Pro	Asp	Pro	Cys				
			420					425					430						
Cys	Phe	Ala	His	Asn	Cys	Ser	Leu	Arg	Ala	Gly	Ala	Gln	Cys	Ala	Gln				
		435					440					445							
Gly	Asp	Cys	Cys	Ala	Arg	Cys	Leu	Leu	Lys	Pro	Ala	Gly	Thr	Pro	Cys				
		450				455					460								
Arg	Pro	Ala	Ala	Asn	Asp	Cys	Asp	Leu	Pro	Glu	Phe	Cys	Thr	Gly	Thr				
465					470					475					480				
Ser	Pro	His	Cys	Pro	Ala	Asp	Val	Tyr	Leu	Leu	Asp	Gly	Ser	Pro	Cys				
				485				490						495					
Ala	Glu	Gly	Arg	Gly	Tyr	Cys	Leu	Asp	Gly	Trp	Cys	Pro	Thr	Leu	Glu				
			500					505						510					
Lys	Gln	Cys	Gln	Gln	Leu	Trp	Gly	Pro	Gly	Ser	Gln	Pro	Ala	Pro	Glu				
		515					520					525							
Pro	Cys	Phe	Gln	Gln	Met	Asn	Ser	Val	Gly	Asn	Ser	Gln	Gly	Asn	Cys				
		530				535					540								
Gly	Gln	Asp	Ser	Lys	Gly	Ser	Phe	Leu	Pro	Cys	Thr	Gln	Arg	Asp	Ala				
545					550														

Gln Gln Pro Gly Arg Cys Cys Arg Arg Asp Ala Leu Cys Asn Arg Asp  
 725 730 735  
 Gln Pro Leu Gly Ser Val His Pro Val Glu Phe Gly Ser Ile Ile Thr  
 740 745 750  
 Gly Glu Pro Ser Pro Pro Asn Pro Glu Glu Ser Glu Leu Thr  
 755 760 765

<210> 498

<211> 609

<212> PRT

<213> Rat

<400> 498

Met Trp Ile Thr Ala Leu Leu Leu Leu Val Leu Leu Leu Val Val Val  
 1 5 10 15  
 His Arg Val Tyr Val Gly Leu Phe Thr Gly Ser Ser Pro Asn Pro Phe  
 20 25 30  
 Ala Glu Asp Val Lys Arg Pro Pro Glu Pro Leu Val Thr Asp Lys Glu  
 35 40 45  
 Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser Val Ser Arg Val Pro  
 50 55 60  
 Glu Lys Leu Asp Ala Val Val Ile Gly Ser Gly Ile Gly Gly Leu Ala  
 65 70 75 80  
 Ser Ala Ala Ile Leu Ala Lys Ala Gly Lys Arg Val Leu Val Leu Glu  
 85 90 95  
 Gln His Thr Lys Ala Gly Gly Cys Cys His Thr Phe Gly Glu Asn Gly  
 100 105 110  
 Leu Glu Phe Asp Thr Gly Ile His Tyr Ile Gly Arg Met Arg Glu Gly  
 115 120 125  
 Asn Ile Gly Arg Phe Ile Leu Asp Gln Ile Thr Glu Gly Gln Leu Asp  
 130 135 140  
 Trp Ala Pro Met Ala Ser Pro Phe Asp Leu Met Ile Leu Glu Gly Pro  
 145 150 155 160  
 Asn Gly Arg Lys Glu Phe Pro Met Tyr Ser Gly Arg Lys Glu Tyr Ile  
 165 170 175  
 Gln Gly Leu Lys Glu Lys Phe Pro Lys Glu Glu Ala Val Ile Asp Lys  
 180 185 190  
 Tyr Met Glu Leu Val Lys Val Val Ala His Gly Val Ser His Ala Ile  
 195 200 205  
 Leu Leu Lys Phe Leu Pro Leu Pro Leu Thr Gln Leu Leu Asn Lys Phe  
 210 215 220  
 Gly Leu Leu Thr Arg Phe Ser Pro Phe Cys Arg Ala Ser Thr Gln Ser  
 225 230 235 240  
 Leu Ala Glu Val Leu Lys Gln Leu Gly Ala Ser Pro Glu Leu Gln Ala  
 245 250 255  
 Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro Ser His Thr  
 260 265 270  
 Thr Phe Ser Leu His Ala Leu Leu Val Asp His Tyr Ile Gln Gly Ala  
 275 280 285  
 Tyr Tyr Pro Arg Gly Gly Ser Ser Glu Ile Ala Phe His Thr Ile Pro  
 290 295 300  
 Leu Ile Gln Arg Ala Gly Gly Ala Val Leu Thr Arg Ala Thr Val Gln  
 305 310 315 320  
 Ser Val Leu Leu Asp Ser Ala Gly Arg Ala Cys Gly Val Ser Val Lys  
 325 330 335  
 Lys Gly Gln Glu Leu Val Asn Ile Tyr Cys Pro Val Val Ile Ser Asn  
 340 345 350

Ala Gly Met Phe Asn Thr Tyr Gln His Leu Leu Pro Glu Ser Val Arg  
 355 360 365  
 Tyr Leu Pro Asp Val Lys Lys Gln Leu Thr Met Val Lys Pro Gly Leu  
 370 375 380  
 Ser Met Leu Ser Ile Phe Ile Cys Leu Lys Gly Thr Lys Glu Glu Leu  
 385 390 395 400  
 Lys Leu Gln Ser Thr Asn Tyr Tyr Val Tyr Phe Asp Thr Asp Met Asp  
 405 410 415  
 Lys Ala Met Glu Arg Tyr Val Ser Met Pro Lys Glu Lys Ala Pro Glu  
 420 425 430  
 His Ile Pro Leu Leu Phe Ile Ala Phe Pro Ser Ser Lys Asp Pro Thr  
 435 440 445  
 Trp Glu Asp Arg Phe Pro Asp Arg Ser Thr Met Thr Val Leu Val Pro  
 450 455 460  
 Thr Ala Phe Glu Trp Phe Glu Glu Trp Gln Glu Glu Pro Lys Gly Lys  
 465 470 475 480  
 Arg Gly Val Asp Tyr Glu Thr Leu Lys Asn Thr Phe Leu Glu Ala Ser  
 485 490 495  
 Met Ser Val Ile Met Lys Leu Phe Pro Gln Leu Glu Gly Lys Val Glu  
 500 505 510  
 Ser Val Thr Gly Gly Ser Pro Leu Thr Asn Gln Tyr Tyr Leu Ala Ala  
 515 520 525  
 His Arg Gly Ala Thr Tyr Gly Ala Asp His Asp Leu Ala Arg Leu His  
 530 535 540  
 Pro His Ala Met Ala Ser Leu Arg Ala Gln Thr Pro Ile Pro Asn Leu  
 545 550 555 560  
 Tyr Leu Thr Gly Gln Asp Ile Phe Thr Cys Gly Leu Met Gly Ala Leu  
 565 570 575  
 Gln Gly Ala Leu Leu Cys Ser Ser Ala Ile Leu Lys Arg Asn Leu Tyr  
 580 585 590  
 Ser Asp Leu Gln Ala Leu Gly Ser Lys Val Arg Ala Gln Lys Lys Lys  
 595 600 605  
 Lys

&lt;210&gt; 499

&lt;211&gt; 559

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 499

Phe Gly Arg Glu Asn Phe Tyr Glu Val Gln Val Pro Glu Asp Thr Pro  
 1 5 10 15  
 Ile Gly Ser Ser Ile Ile Thr Ile Ser Ala Lys Asp Leu Asp Met Gly  
 20 25 30  
 Asn Tyr Gly Lys Ile Ser Tyr Ser Phe Leu His Ala Thr Glu Asp Val  
 35 40 45  
 Arg Lys Thr Phe Glu Ile Asn Pro Thr Ser Gly Glu Val Asn Leu Arg  
 50 55 60  
 Ser Leu Leu Asp Phe Glu Val Ile Gln Ser Tyr Ser Val Thr Ile Gln  
 65 70 75 80  
 Ala Thr Asp Gly Gly Glu Leu Ser Ala Lys Cys Thr Leu Ser Val Lys  
 85 90 95  
 Val Leu Asp Ile Asn Asp Asn Ala Pro Glu Val Ile Ile Ser Ser Val  
 100 105 110  
 Thr Lys Thr Ile Pro Glu Asn Ala Ser Glu Thr Leu Ile Thr Leu Phe  
 115 120 125

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Ser Val Arg Asp Gln Asp Ser Gly Asp Asn Gly Arg Ile Leu Cys Ser
130 135 140
Ile Pro Asp Asp Leu Pro Phe Ile Leu Lys Pro Thr Phe Lys Asn Phe
145 150 155 160
Phe Thr Leu Leu Ser Glu Lys Ala Leu Asp Arg Glu Ser Arg Ala Glu
165 170 175
Tyr Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr Pro Arg Leu Thr
180 185 190
Thr Gln His Thr Ile Thr Val Gln Val Ser Asp Ile Asn Asp Asn Ala
195 200 205
Pro Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val His Glu Asn Asn
210 215 220
Ser Pro Ala Leu His Ile Glu Thr Ile Ser Ala Thr Asp Ser Asp Ser
225 230 235 240
Gly Ser Asn Ala His Ile Thr Tyr Ser Leu Met Pro Pro Arg Asp Pro
245 250 255
Gln Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Ala Asp Asn Gly Gln
260 265 270
Leu Phe Ala Leu Arg Ala Leu Asp Tyr Glu Val Leu Gln Ala Phe Glu
275 280 285
Phe Arg Val Gly Ala Thr Asp Arg Gly Ser Pro Ala Leu Ser Ser Gln
290 295 300
Ala Leu Val Arg Val Val Val Leu Asp Asp Asn Asp Asn Ala Pro Phe
305 310 315 320
Val Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Tyr Thr Glu Leu Leu
325 330 335
Pro Arg Ala Ala Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val
340 345 350
Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe Gln Leu Leu Lys
355 360 365
Ala Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His Asn Gly Glu Val
370 375 380
Arg Thr Ser Arg Leu Leu Ser Glu Arg Asp Ala Pro Lys His Lys Leu
385 390 395 400
Leu Leu Met Val Lys Asp Asn Gly Asp Pro Pro Arg Ser Ala Ser Val
405 410 415
Met Leu His Val Leu Val Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro
420 425 430
Leu Pro Glu Val Ala His Asn Pro Ala His Asp Glu Asp Thr Leu Thr
435 440 445
Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
450 455 460
Ser Val Leu Leu Phe Val Gly Val Arg Leu Cys Lys Lys Ala Arg Ala
465 470 475 480
Ala Ser Leu Gly Gly Cys Ser Val Pro Glu Gly His Phe Pro Gly His
485 490 495
Leu Val Asp Val Thr Gly Thr Gly Thr Leu Ser Gln Asn Tyr Gln Tyr
500 505 510
Glu Val Cys Leu Thr Gly Ser Thr Gly Thr Asn Glu Phe Lys Phe Leu
515 520 525
Lys Pro Val Met Pro Ser Leu Gln Leu Gln Asp Pro Asp Ser Asn Met
530 535 540
Leu Val Lys Glu Asn Phe Arg Asn Ser Leu Gly Phe Asn Ile Gln
545 550 555

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&lt;210&gt; 500

&lt;211&gt; 545

<212> PRT  
<213> Mouse

<400> 500

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Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
 1          5          10          15
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
          20          25          30
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
          35          40          45
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
          50          55          60
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
          65          70          75          80
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu Asp Thr
          85          90          95
Ala Asp Tyr Val Lys Pro Val Ala Phe Ser Val Glu Tyr Ser Leu Glu
          100          105          110
Asp Pro Asp His Gly Pro Met Leu Asp Asn Gly Trp Pro Thr Thr Leu
          115          120          125
Arg Val Ser Val Pro Phe Trp Asn Gly Cys Asn Glu Asp Glu His Cys
          130          135          140
Val Pro Asp Leu Val Leu Asp Ala Arg Ser Asp Leu Pro Thr Ala Met
          145          150          155          160
Glu Tyr Cys Gln Gln Val Leu Arg Arg Pro Ala Gln Asp Cys Ser Ser
          165          170          175
Tyr Thr Leu Ser Phe Asp Thr Thr Val Phe Ile Ile Glu Ser Thr Arg
          180          185          190
Arg Arg Val Ala Val Glu Ala Thr Leu Glu Asn Arg Gly Glu Asn Ala
          195          200          205
Tyr Ser Ala Val Leu Asn Ile Ser Gln Ser Glu Asn Leu Gln Phe Ala
          210          215          220
Ser Leu Ile Gln Lys Asp Asp Ser Asp Asn Ser Ile Glu Cys Val Asn
          225          230          235          240
Glu Glu Arg Arg Leu His Lys Lys Val Cys Asn Val Ser Tyr Pro Phe
          245          250          255
Phe Arg Ala Lys Ala Lys Val Ala Phe Arg Leu Asp Phe Glu Phe Ser
          260          265          270
Lys Ser Val Phe Leu His His Leu Gln Ile His Leu Gly Ala Gly Ser
          275          280          285
Asp Ser His Glu Gln Asp Ser Thr Ala Asp Asp Asn Thr Ala Leu Leu
          290          295          300
Arg Phe His Leu Lys Tyr Glu Ala Asp Val Leu Phe Thr Arg Ser Ser
          305          310          315          320
Ser Leu Ser His Phe Glu Val Lys Ala Asn Ser Ser Leu Glu Ser Tyr
          325          330          335
Asp Gly Ile Gly Pro Pro Phe Asn Cys Val Phe Lys Val Gln Asn Leu
          340          345          350
Gly Phe Phe Pro Ile His Gly Val Met Met Lys Ile Thr Val Pro Ile
          355          360          365
Ala Thr Arg Gly Gly Asn Arg Leu Leu Met Leu Lys Asp Phe Phe Thr
          370          375          380
Asp Gln Val Asn Thr Ser Cys Asn Ile Trp Gly Asn Ser Thr Glu Tyr
          385          390          395          400
Arg Ser Thr Pro Thr Glu Glu Asp Leu Ser His Ala Pro Gln Arg Asn
          405          410          415
His Ser Asn Ser Asp Val Val Ser Ile Ile Cys Asn Val Arg Leu Ala

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          420          425          430
Pro Asn Gln Glu Thr Ser Phe Tyr Leu Val Gly Asn Leu Trp Leu Met
          435          440          445
Ser Leu Lys Ala Leu Lys Tyr Arg Ser Met Lys Ile Thr Val Asn Ala
          450          455          460
Ala Leu Gln Arg Gln Phe His Ser Pro Phe Ile Phe Arg Glu Glu Asp
465          470          475          480
Pro Ser Arg Gln Val Thr Phe Glu Ile Ser Lys Gln Glu Asp Trp Gln
          485          490          495
Val Pro Ile Trp Ile Ile Val Gly Ser Ser Leu Gly Gly Leu Leu Leu
          500          505          510
Leu Ala Leu Leu Val Leu Ala Leu Trp Lys Leu Gly Phe Phe Lys Ser
          515          520          525
Ala Lys Arg Lys Arg Glu Pro Ser Leu Gly Pro Val Pro Lys Glu Leu
          530          535          540
Glu
545

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<210> 501
<211> 696
<212> PRT
<213> Rat

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          <400> 501
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
1          5          10          15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
          20          25          30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
          35          40          45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
          50          55          60
Pro Leu Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65          70          75          80
Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser Glu
          85          90          95
Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln Leu
          100          105          110
Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu Gly
          115          120          125
Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala Ser
          130          135          140
Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys Lys
145          150          155          160
Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe Gly
          165          170          175
Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile Arg
          180          185          190
Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His Leu
          195          200          205
Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser Ser
          210          215          220
Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu Asp Thr Ala
225          230          235          240
Asp Tyr Val Lys Pro Val Ala Phe Ser Val Glu Tyr Ser Leu Glu Asp
          245          250          255
Pro Asp His Gly Pro Met Leu Asp Asn Gly Trp Pro Thr Thr Leu Arg

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Val	Ser	Val	Pro	Phe	Trp	Asn	Gly	Cys	Asn	Glu	Asp	Glu	His	Cys	Val
		275					280					285			
Pro	Asp	Leu	Val	Leu	Asp	Ala	Arg	Ser	Asp	Leu	Pro	Thr	Ala	Met	Glu
		290				295					300				
Tyr	Cys	Gln	Gln	Val	Leu	Arg	Arg	Pro	Ala	Gln	Asp	Cys	Ser	Ser	Tyr
305					310					315					320
Thr	Leu	Ser	Phe	Asp	Thr	Thr	Val	Phe	Ile	Ile	Glu	Ser	Thr	Arg	Arg
				325					330					335	
Arg	Val	Ala	Val	Glu	Ala	Thr	Leu	Glu	Asn	Arg	Gly	Glu	Asn	Ala	Tyr
			340					345					350		
Ser	Ala	Val	Leu	Asn	Ile	Ser	Gln	Ser	Glu	Asn	Leu	Gln	Phe	Ala	Ser
		355					360					365			
Leu	Ile	Gln	Lys	Asp	Asp	Ser	Asp	Asn	Ser	Ile	Glu	Cys	Val	Asn	Glu
		370				375					380				
Glu	Arg	Arg	Leu	His	Lys	Lys	Val	Cys	Asn	Val	Ser	Tyr	Pro	Phe	Phe
385					390					395					400
Arg	Ala	Lys	Ala	Lys	Val	Ala	Phe	Arg	Leu	Asp	Phe	Glu	Phe	Ser	Lys
			405						410					415	
Ser	Val	Phe	Leu	His	His	Leu	Gln	Ile	His	Leu	Gly	Ala	Gly	Ser	Asp
			420					425					430		
Ser	His	Glu	Gln	Asp	Ser	Thr	Ala	Asp	Asp	Asn	Thr	Ala	Leu	Leu	Arg
		435					440					445			
Phe	His	Leu	Lys	Tyr	Glu	Ala	Asp	Val	Leu	Phe	Thr	Arg	Ser	Ser	Ser
		450				455					460				
Leu	Ser	His	Phe	Glu	Val	Lys	Ala	Asn	Ser	Ser	Leu	Glu	Ser	Tyr	Asp
465					470					475					480
Gly	Ile	Gly	Pro	Pro	Phe	Asn	Cys	Val	Phe	Lys	Val	Gln	Asn	Leu	Gly
			485						490					495	
Phe	Phe	Pro	Ile	His	Gly	Val	Met	Met	Lys	Ile	Thr	Val	Pro	Ile	Ala
		500						505					510		
Thr	Arg	Gly	Gly	Asn	Arg	Leu	Leu	Met	Leu	Lys	Asp	Phe	Phe	Thr	Asp
		515					520					525			
Gln	Val	Asn	Thr	Ser	Cys	Asn	Ile	Trp	Gly	Asn	Ser	Thr	Glu	Tyr	Arg
		530				535					540				
Ser	Thr	Pro	Thr	Glu	Glu	Asp	Leu	Ser	His	Ala	Pro	Gln	Arg	Asn	His
545					550					555					560
Ser	Asn	Ser	Asp	Val	Val	Ser	Ile	Ile	Cys	Asn	Val	Arg	Leu	Ala	Pro
			565						570					575	
Asn	Gln	Glu	Thr	Ser	Phe	Tyr	Leu	Val	Gly	Asn	Leu	Trp	Leu	Met	Ser
		580						585					590		
Leu	Lys	Ala	Leu	Lys	Tyr	Arg	Ser	Met	Lys	Ile	Thr	Val	Asn	Ala	Ala
		595					600					605			
Leu	Gln	Arg	Gln	Phe	His	Ser	Pro	Phe	Ile	Phe	Arg	Glu	Glu	Asp	Pro
		610				615					620				
Ser	Arg	Gln	Val	Thr	Phe	Glu	Ile	Ser	Lys	Gln	Glu	Asp	Trp	Gln	Val
625					630					635					640
Pro	Ile	Trp	Ile	Ile	Val	Gly	Ser	Ser	Leu	Gly	Gly	Leu	Leu	Leu	Leu
			645						650					655	
Ala	Leu	Leu	Val	Leu	Ala	Leu	Gly	Ser	Leu	Val	Ser	Leu	Lys	Val	Pro
		660						665					670		
Ser	Ala	Arg	Gly	Ser	Pro	Ala	Trp	Ala	Pro	Ser	Pro	Lys	Ser	Trp	Ser
		675					680					685			
Glu	Asp	Pro	Glu	Glu	Ala	Ser	Ser								
		690				695									

&lt;210&gt; 502

<211> 242  
 <212> PRT  
 <213> Rat

<400> 502

Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln  
 1 5 10 15  
 Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val  
 20 25 30  
 Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu  
 35 40 45  
 Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys  
 50 55 60  
 Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala  
 65 70 75 80  
 Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys  
 85 90 95  
 Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg Cys Lys  
 100 105 110  
 Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val  
 115 120 125  
 Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu  
 130 135 140  
 Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln  
 145 150 155 160  
 Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe  
 165 170 175  
 Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe  
 180 185 190  
 Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp  
 195 200 205  
 Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly  
 210 215 220  
 Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys  
 225 230 235 240  
 Gly Arg

<210> 503  
 <211> 819  
 <212> PRT  
 <213> Rat

<400> 503

Lys Ser Trp Thr Ile Ile Gln Glu Arg Leu Gln Met Asp Ser Met Val  
 1 5 10 15  
 Ile Lys Gly Leu Asp Pro Asp Thr Asn Tyr Gln Phe Ala Val Arg Ala  
 20 25 30  
 Met Asn Ala Tyr Gly Phe Ser Leu Arg Ser Gln Pro Ser Asn Thr Ile  
 35 40 45  
 Arg Thr Leu Gly Pro Gly Glu Ala Gly Ser Gly Arg Tyr Gly Pro Gly  
 50 55 60  
 Tyr Ile Thr Asp Thr Gly Val Ser Glu Asp Asp Ala Ser Glu Asp  
 65 70 75 80  
 Glu Leu Asp Leu Asp Val Ser Phe Glu Glu Val Lys Pro Leu Pro Ala  
 85 90 95  
 Thr Lys Val Gly Asn Lys Lys Ser Lys Lys Thr Ser Val Ser Asn Ser

[illegible]

```

Ile Leu His Pro Phe Ser Gly Ser Ile Gln Lys Ile Ile Leu Asn Asp
565 570 575
Arg Thr Ile His Val Arg His Asp Phe Thr Ser Gly Val Asn Val Glu
580 585 590
Asn Ala Ala His Pro Cys Val Gly Ala Pro Cys Ala His Gly Gly Ser
595 600 605
Cys Arg Pro Arg Lys Glu Gly Tyr Glu Cys Asp Cys Pro Leu Gly Phe
610 615 620
Glu Gly Leu Asn Cys Gln Lys Ala Ile Thr Glu Ala Ile Glu Ile Pro
625 630 635 640
Gln Phe Ile Gly Arg Ser Tyr Leu Thr Tyr Asp Asn Pro Asn Ile Leu
645 650 655
Lys Arg Val Ser Gly Ser Arg Ser Asn Ala Phe Met Arg Phe Lys Thr
660 665 670
Thr Ala Lys Asp Gly Leu Leu Leu Trp Arg Gly Asp Ser Pro Met Arg
675 680 685
Pro Asn Ser Asp Phe Ile Ser Leu Gly Leu Arg Asp Gly Ala Leu Val
690 695 700
Phe Ser Tyr Asn Leu Gly Ser Gly Val Ala Ser Ile Met Val Asn Gly
705 710 715 720
Ser Phe Ser Asp Gly Arg Trp His Arg Val Lys Ala Val Arg Asp Gly
725 730 735
Gln Ser Gly Lys Ile Thr Val Asp Asp Tyr Gly Ala Arg Thr Gly Lys
740 745 750
Ser Pro Gly Met Met Arg Gln Leu Asn Ile Asn Gly Ala Leu Tyr Val
755 760 765
Gly Gly Met Lys Glu Ile Ala Leu His Thr Asn Arg Gln Tyr Met Arg
770 775 780
Gly Leu Val Gly Cys Ile Ser His Phe Thr Leu Ser Thr Asp Tyr His
785 790 795 800
Ile Ser Leu Val Glu Asp Ala Val Asp Gly Lys Asn Ile Asn Thr Cys
805 810 815
Gly Ala Lys

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<210> 504
<211> 127
<212> PRT
<213> Rat

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```

<400> 504
Gly Glu Arg Gly Pro Lys Gly Glu Lys Gly Glu Arg Gly Glu Arg Ala
1 5 10 15
Ala Gly Asp Met Asp Phe Thr Met Ile Arg Leu Val Asn Gly Ser Gly
20 25 30
Pro His Gln Gly Arg Val Glu Val Phe His Asp Arg Arg Trp Gly Thr
35 40 45
Val Cys Asp Asp Gly Trp Asp Lys Lys Asp Gly Asp Val Val Cys Arg
50 55 60
Met Leu Gly Phe His Ser Val Glu Glu Val His Arg Thr Ala Arg Phe
65 70 75 80
Gly Gln Gly Thr Gly Arg Ile Trp Met Asp Asp Val Asn Cys Lys Gly
85 90 95
Thr Glu Ser Ser Ile Phe His Cys Gln Phe Ser Lys Trp Gly Val Thr
100 105 110
Asn Cys Gly His Ala Glu Asp Ala Gly Val Thr Cys Thr Ala Leu
115 120 125

```

<210> 505  
 <211> 125  
 <212> PRT  
 <213> Human

<400> 505  
 Ser Leu His Ser Cys His Leu Glu Arg Ile Ser Arg Gly Ala Phe Gln  
 1 5 10 15  
 Glu Gln Gly His Leu Arg Ser Leu Val Leu Gly Asp Asn Cys Leu Ser  
 20 25 30  
 Glu Asn Tyr Glu Glu Thr Ala Ala Leu His Ala Leu Pro Gly Leu  
 35 40 45  
 Arg Arg Leu Asp Leu Ser Gly Asn Ala Leu Thr Glu Asp Met Ala Ala  
 50 55 60  
 Leu Met Leu Gln Asn Leu Ser Ser Leu Arg Ser Val Ser Leu Ala Gly  
 65 70 75 80  
 Asn Thr Ile Met Arg Leu Asp Asp Ser Val Phe Glu Gly Leu Glu Arg  
 85 90 95  
 Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr Ile Phe Glu Ile Glu Gly  
 100 105 110  
 Gly Ala Phe Asp Gly Leu Ala Glu Leu Arg His Leu Asn  
 115 120 125

<210> 506  
 <211> 551  
 <212> PRT  
 <213> Rat

<400> 506  
 Met Gln Pro Pro Trp Gly Leu Ala Leu Pro Leu Leu Leu Pro Trp Val  
 1 5 10 15  
 Ala Gly Gly Val Gly Thr Ser Pro Arg Asp Tyr Trp Leu Pro Ala Leu  
 20 25 30  
 Ala His Gln Pro Gly Val Cys His Tyr Gly Thr Lys Thr Ala Cys Cys  
 35 40 45  
 Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val Cys Glu Ala Val Cys Glu  
 50 55 60  
 Pro Arg Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys  
 65 70 75 80  
 Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys  
 85 90 95  
 Ala Phe Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly  
 100 105 110  
 Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Leu Pro Asp Ala  
 115 120 125  
 Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg Ile Asn Cys Gln Tyr Ser  
 130 135 140  
 Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys Val Cys Pro Ser Ser Gly  
 145 150 155 160  
 Leu Arg Leu Gly Pro Asn Gly Arg Val Cys Leu Asp Ile Asp Glu Cys  
 165 170 175  
 Ala Ser Ser Lys Ala Val Cys Pro Ser Asn Arg Arg Cys Val Asn Thr  
 180 185 190  
 Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Lys Tyr  
 195 200 205  
 Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile Asn Glu Cys Thr Leu Asn

```

      210      215      220
Thr Arg Thr Cys Ser Pro His Ala Asn Cys Leu Asn Thr Gln Gly Ser
225      230      235
Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg Gly Asn Gly Leu Gln Cys
      245      250      255
Ser Val Ile Pro Glu His Ser Val Lys Glu Ile Leu Thr Ala Pro Gly
      260      265      270
Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys His Thr Met
      275      280      285
Lys Lys Lys Val Lys Leu Lys Asn Val Thr Pro Arg Pro Thr Ser Thr
      290      295      300
Arg Ala Pro Lys Val Asn Leu Pro Tyr Ser Ser Glu Glu Gly Val Ser
305      310      315      320
Arg Gly Arg Asn Ser Gly Gly Glu Gln Lys Arg Lys Glu Glu Arg Lys
      325      330      335
Arg Lys Arg Leu Glu Glu Glu Lys Ser Glu Lys Ala Leu Arg Asn Glu
      340      345      350
Val Glu Gln Glu Arg Pro Leu Arg Gly Asp Val Phe Ser Pro Lys Val
      355      360      365
Asn Glu Ala Glu Asp Leu Asp Leu Val Tyr Ile Gln Arg Lys Glu Leu
      370      375      380
Asn Ser Lys Gln Glu His Lys Ala Asp Leu Asn Ile Ser Val Asp Cys
385      390      395      400
Ser Phe Asp Leu Gly Val Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp
      405      410      415
Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Asp Val Gly Tyr Tyr Met
      420      425      430
Ala Val Pro Ala Leu Ala Gly His Lys Lys Asn Ile Gly Arg Leu Lys
      435      440      445
Leu Leu Leu Pro Asn Leu Thr Pro Gln Ser Asn Phe Cys Leu Leu Phe
      450      455      460
Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val
      465      470      475      480
Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Glu Thr Lys Thr Glu Asp
      485      490      495
Gly Lys Trp Lys Thr Gly Lys Val Pro Leu Tyr Gln Gly Ile Asp Thr
      500      505      510
Thr Lys Ser Val Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly
      515      520      525
Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp
      530      535      540
Asp Phe Leu Ser Glu Glu Gly
545      550

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<210> 507
<211> 244
<212> PRT
<213> Mouse

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      <400> 507
Tyr Ala Ser Ala Ser Glu Pro Thr Glu Ile Tyr Arg Thr Glu Leu Gln
1      5      10      15
Gly Leu Trp Ile Asn Asp Ile Val Pro Ile Gly Arg Ile Gln Glu Pro
      20      25      30
Ala His Leu Asp Phe Met Cys Leu Gln Asn Glu Val Tyr Lys Gln Thr
      35      40      45
Glu Gln Leu Ala Glu Leu Ser Lys Gly Val Gln Glu Val Val Leu Ser

```

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      50      55      60
Ser Ile Leu Ser Met Leu Tyr Glu Gly Asp Arg Lys Val Leu Tyr Asp
65      70      75      80
Leu Met Asn Met Leu Glu Leu Asn Gln Leu Gly His Met Asp Gly Pro
      85      90      95
Gly Gly Lys Ile Leu Asp Glu Leu Arg Lys Asp Ser Ser Asn Pro Cys
100      105      110
Val Asp Leu Lys Asp Leu Ile Leu Tyr Leu Leu Gln Ala Leu Met Val
115      120      125
Leu Ser Asp Ser Gln Leu Asn Leu Leu Ala Gln Ser Val Glu Met Gly
130      135      140
Ile Leu Pro His Gln Val Glu Leu Val Lys Ser Ile Leu Gln Pro Asn
145      150      155      160
Phe Lys Tyr Pro Trp Asn Ile Pro Phe Thr Val Gln Pro Gln Leu Leu
165      170      175
Ala Pro Leu Gln Gly Glu Gly Leu Ala Ile Thr Tyr Glu Leu Leu Glu
180      185      190
Glu Cys Gly Leu Lys Met Glu Leu Asn Asn Pro Arg Ser Thr Trp Asp
195      200      205
Leu Glu Ala Lys Met Pro Leu Ser Ala Leu Tyr Gly Ser Leu Ser Phe
210      215      220
Leu Gln Gln Leu Arg Lys Ala Asn Ser Ser Ser Lys Pro Ser Leu Arg
225      230      235      240
Pro Gly Tyr Ile

```

```

<210> 508
<211> 248
<212> PRT
<213> Human

```

```

      <400> 508
Val Ser Cys Arg Tyr Leu Lys Asn Ser Leu His Val Phe Val Ser Gly
1      5      10      15
Gly Ala Ile Gly Thr Ser Ser Pro Ala Leu Leu Glu Cys Gln Glu Gly
20      25      30
Val Gly Pro Ala Arg Pro Ser Leu Val Pro Pro Pro Arg Pro
35      40      45
Arg Arg Leu Asp Leu Ala Arg Thr Leu Pro Ala Glu Arg Thr Asp Ser
50      55      60
Gln Ser Leu Tyr Ile Val Tyr Ile Ala Leu Pro Gly Arg Thr Pro Arg
65      70      75      80
Pro Ala Leu Ala Phe Ala Phe Leu Met Pro Ala Cys Cys Asn Arg Pro
85      90      95
Ser Pro Arg Pro Ser Pro Ala His Leu Thr Ala Ser Ser Val Leu Arg
100      105      110
Arg Gln Arg His Val Leu Ala Ala Ser Ala Ala Ser Pro Cys Gln Trp
115      120      125
Ser Gly Leu Arg Val Ala His Ser Leu Arg Gln Val Val Ser Leu Cys
130      135      140
Pro Arg Cys Thr Gly Ser Cys Pro Phe Ser Gly Ala Cys Ala Ser Ser
145      150      155      160
Leu Pro Ser Pro Leu Ser Cys Pro His Ser His Ser Gly Ser Trp Gly
165      170      175
Thr Trp Ser Gln Gly Arg Pro Cys Ser Ser Thr Glu Val Ala Gly Leu
180      185      190
Ala Leu Trp Pro Thr Asp Phe Leu Ser Cys Leu Leu Asp Ala Ser Glu

```

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      195              200              205
Leu Gln Thr Gln Gly Ser His Gly Phe Ser Phe Thr Pro Thr Gly Phe
  210              215              220
Ser Ser Asn Arg Lys Val Gly Val Gly Ser Cys Arg Asp Gly Ala Gly
  225              230              235              240
Arg Gly Ala Met Gly Gly Leu Phe
      245

```

```

<210> 509
<211> 698
<212> PRT
<213> Mouse

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```

      <400> 509
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Asn Pro
  1              5              10              15
Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
      20              25              30
Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
  35              40              45
Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
  50              55              60
Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
  65              70              75              80
Ala Leu Cys Val Arg Val Val Val His Leu Ala Val His Gly His Trp
      85              90              95
Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
      100              105              110
Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
      115              120              125
Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
  130              135              140
Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
  145              150              155              160
Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
      165              170              175
Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Cys Arg Gly
      180              185              190
Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp Val Leu Pro Trp Leu
      195              200              205
Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu Thr Leu Asp Val Ser
  210              215              220
Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu Arg Pro Val Pro Asp
  225              230              235              240
Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr Gly Pro Gln Asn Ile
      245              250              255
Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp
      260              265              270
Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe Cys Pro Phe Arg Glu
      275              280              285
Asp Pro Gly Ala His Arg Asn Leu Trp His Ile Ala Arg Leu Arg Val
  290              295              300
Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro Cys Cys Leu Pro Gly
  305              310              315              320
Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln Ser Pro Cys Gln Pro
      325              330              335
Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr Val Asn Glu Pro Gln

```



Asp	Phe	Gln	Leu	Val	Ala	Gly	His	Pro	Asn	Leu	Cys	Val	Gln	Val	Ser
		340						345					350		
Thr	Trp	Glu	Lys	Val	Gln	Leu	Gln	Ala	Cys	Leu	Trp	Ala	Asp	Ser	Leu
		355					360					365			
Gly	Pro	Phe	Lys	Asp	Asp	Met	Leu	Leu	Val	Glu	Met	Lys	Thr	Gly	Leu
		370				375					380				
Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys	Thr	Pro	Leu
				405					410					415	
Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	Glu	Leu	Leu
			420					425					430		
Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	Trp	Asn	Asp	Asp	Asn
		435					440					445			
Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	Arg	Arg
		450				455					460				
Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Phe
					470				475						480
Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Ser
				485					490					495	
Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	Gly	Tyr	Glu	Arg
			500					505					510		
Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	Met	Pro	Leu	Arg	Val
		515					520					525			
Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	His	Gly	Ala	Leu
		530				535					540				
Ala	Trp	Phe	His	His	Gln	Arg	Arg	Ile	Leu	Gln	Glu	Gly	Gly	Val	
					550				555					560	
Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala	Gln	Cys	Gln	Gln	Trp
				565					570					575	
Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His	Asp	Ala	Leu	Ala	Ala
			580					585					590		
Trp	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg	Ala	Thr	Gly
		595					600					605			
Arg	Tyr	Val	Gly	Val	Tyr	Phe	Asp	Gly	Leu	Leu	His	Pro	Asp	Ser	Val
		610				615					620				
Pro	Ser	Pro	Phe	Arg	Val	Ala	Pro	Leu	Phe	Ser	Leu	Pro	Ser	Gln	Leu
		625			630				635					640	
Pro	Ala	Phe	Leu	Asp	Ala	Leu	Gln	Gly	Gly	Cys	Ser	Thr	Ser	Ala	Gly
				645					650					655	
Arg	Pro	Ala	Asp	Arg	Val	Glu	Arg	Val	Thr	Gln	Ala	Leu	Arg	Ser	Ala
			660					665					670		
Leu	Asp	Ser	Cys	Thr	Ser	Thr	Ser	Glu	Ala	Pro	Gly	Cys	Cys	Glu	Glu
		675					680					685			
Trp	Asp	Leu	Gly	Pro	Cys	Thr	Thr	Leu	Glu						
		690				695									

<210> 510  
 <211> 1700  
 <212> DNA  
 <213> Rat

<400> 1  
 cctttttgtgg cacacccagg gccagttac ttctcaggtt cgagtctaaa ctctcagccg  
 tagacgttgt agacgtcggg gttccagctc catcttttga cacataatcc aggaagccgc  
 tagctctcga tgtcttctgt caagttatgg ctcaatgggt cgtcacgat ctctctcgtg  
 ggctctgaag aactggagaa cctaggattt gtgggcaaag gcgggttcgg agccgtgttc  
 cgggcacgcc acacagcatg gaaccttgat gttagcagtc agatcgtgaa ctogaagaag

atatccaggg	agggtgaaggc	tatggtgaat	cttcgtcatg	agaacgtgct	gtccctgctg	360
ggggtcactg	agaacctcga	gtgggactac	gtgtacgggc	cggctctggt	gacaggattc	420
atggagaacg	gctccctctc	agggctgctg	caaccttcat	gcctcggcc	ctggcctctc	480
ctctgtcgcc	tgctagagga	agtgggtgctg	gggatgtgct	acctacacag	cttgaacctc	540
tcgctactgc	accgggacct	caagccctcc	aatgttctgc	tggatccaga	gtccacgcgc	600
aagttagcag	actttggcct	gtccacattt	cagggagggt	cacagtcagg	gtcagggtca	660
ggatcgagag	attctggggg	caccctagct	tacttggccc	cagagctggt	ggataatgac	720
ggaaaggcct	ctaaagcaag	tgatgtttac	agttttgggg	tcctcggtg	gacagtgcctg	780
gctggaagag	aagctgaggt	ggtagacaag	acctcactaa	ttcgtggagc	agtgtgtaac	840
aggcagaggc	gacctccatt	gacagagctg	cctccggaca	gccttgagac	tcctggcctta	900
gaaggactga	aggagttaat	gacgcattgc	tggagttctg	agcctaaaga	caggccatcc	960
ttccaagact	gtgaatcaaa	aaccaataat	gtttacatoc	tggtagagga	caaggtagat	1020
gctgctgtct	ccaaggtaaa	gcattatctg	tctcagtaca	gaagcagtga	cacaaagtgt	1080
tcctgccagag	agtccagcca	aaaagggtaca	gaggtggatt	gccccaggga	aaccatagtt	1140
tatgaaatgc	tggaaccgct	gcactctggag	gagccctctg	gatcagttcc	tgaaagactc	1200
acaagtctta	ctgagaggag	aggaaaggaa	gcatactttg	ggcatgccac	accagcaggg	1260
acatcatctg	acaccttggc	tggcactccc	caaattccac	atactttacc	ctccagagggc	1320
acaacaccta	ggccagcctt	tactgagact	ccaggtcctg	acccccaaag	gaatcaggga	1380
gatggaagaa	acagcaatcc	ttggtacacc	tggaaacgcac	caaattccaat	gacagggtca	1440
cagtctattg	tcttaaacaa	ctgttctgaa	gtgcagattg	gacaacacaa	ctgcattgtca	1500
gtacaaccga	gaactgcctt	tcccaagaag	gagccagcac	agttcggcag	gggtaggggc	1560
tggtagcccg	tccacgtcca	cgagtagact	tcggagagga	cctgcaagtg	cctgaagcag	1620
gaaatacacc	attcaggcag	ccagtataaa	tagagtgaag	ataaaaagcac	tttctaagca	1680
aaaaaaaaaa	aaaaaaaaaa					1700

<210> 511  
 <211> 2538  
 <212> DNA  
 <213> Rat

<400> 2						
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&lt;210&gt; 512

&lt;211&gt; 478

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 3

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20      25      30
Phe Gly Ala Val Phe Arg Ala Arg His Thr Ala Trp Asn Leu Asp Val
35      40      45
Ala Val Lys Ile Val Asn Ser Lys Lys Ile Ser Arg Glu Val Lys Ala
50      55      60
Met Val Asn Leu Arg His Glu Asn Val Leu Leu Leu Leu Gly Val Thr
65      70      75      80
Glu Asn Leu Glu Trp Asp Tyr Val Tyr Gly Pro Ala Leu Val Thr Gly
85      90      95
Phe Met Glu Asn Gly Ser Leu Ser Gly Leu Leu Gln Pro Ser Cys Pro
100      105      110
Arg Pro Trp Pro Leu Leu Cys Arg Leu Leu Glu Glu Val Val Leu Gly
115      120      125
Met Cys Tyr Leu His Ser Leu Asn Pro Ser Leu Leu His Arg Asp Leu
130      135      140
Lys Pro Ser Asn Val Leu Leu Asp Pro Glu Leu His Ala Lys Leu Ala
145      150      155      160
Asp Phe Gly Leu Ser Thr Phe Gln Gly Gly Ser Gln Ser Gly Ser Gly
165      170      175
Ser Gly Ser Arg Asp Ser Gly Gly Thr Leu Ala Tyr Leu Ala Pro Glu
180      185      190
Leu Leu Asp Asn Asp Gly Lys Ala Ser Lys Ala Ser Asp Val Tyr Ser
195      200      205
Phe Gly Val Leu Val Trp Thr Val Leu Ala Gly Arg Glu Ala Glu Val
210      215      220
Val Asp Lys Thr Ser Leu Ile Arg Gly Ala Val Cys Asn Arg Gln Arg
225      230      235      240
Arg Pro Pro Leu Thr Glu Leu Pro Pro Asp Ser Pro Glu Thr Pro Gly
245      250      255
Leu Glu Gly Leu Lys Glu Leu Met Thr His Cys Trp Ser Ser Glu Pro

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Tyr Ile Leu Val Gln Asp Lys Val Asp Ala Ala Val Ser Lys Val Lys
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His Tyr Leu Ser Gln Tyr Arg Ser Ser Asp Thr Lys Leu Ser Ala Arg
305                310                315                320
Glu Ser Ser Gln Lys Gly Thr Glu Val Asp Cys Pro Arg Glu Thr Ile
325                330                335
Val Tyr Glu Met Leu Asp Arg Leu His Leu Glu Glu Pro Ser Gly Ser
340                345                350
Val Pro Glu Arg Leu Thr Ser Leu Thr Glu Arg Arg Gly Lys Glu Ala
355                360                365
Ser Phe Gly His Ala Thr Pro Ala Gly Thr Ser Ser Asp Thr Leu Ala
370                375                380
Gly Thr Pro Gln Ile Pro His Thr Leu Pro Ser Arg Gly Thr Thr Pro
385                390                395                400
Arg Pro Ala Phe Thr Glu Thr Pro Gly Pro Asp Pro Gln Arg Asn Gln
405                410                415
Gly Asp Gly Arg Asn Ser Asn Pro Trp Tyr Thr Trp Asn Ala Pro Asn
420                425                430
Pro Met Thr Gly Leu Gln Ser Ile Val Leu Asn Asn Cys Ser Glu Val
435                440                445
Gln Ile Gly Gln His Asn Cys Met Ser Val Gln Pro Arg Thr Ala Phe
450                455                460
Pro Lys Lys Glu Pro Ala Gln Phe Gly Arg Gly Arg Gly Trp
465                470                475

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&lt;210&gt; 513

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 4

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20                25                30
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35                40                45
Ala Lys His Gly Glu Glu Leu Lys Val Leu Lys Glu Ile Ser Val Gly
50                55                60
Glu Leu Asn Pro Asn Glu Ser Val Gln Ala Ser Met Glu Ala Gln Leu
65                70                75                80
Leu Ser Thr Leu Asn His Pro Ala Ile Val Arg Phe His Ala Ser Phe
85                90                95
Met Glu Gln Gly Thr Phe Cys Ile Ile Thr Glu Tyr Cys Glu Gly Arg
100                105                110
Asp Leu Asp Tyr Lys Ile Gln Glu Tyr Lys Glu Ala Gly Lys Ile Phe
115                120                125
Pro Asp Asn Gln Ile Val Glu Trp Phe Ile Gln Leu Leu Leu Gly Val
130                135                140
Asp Tyr Met His Glu Arg Arg Ile Leu His Arg Asp Leu Lys Ser Lys
145                150                155                160
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165                170                175
Ser Arg Leu Leu Met Gly Ser Cys Glu Leu Ala Thr Thr Leu Thr Gly

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 Lys Ile Thr Glu Gly Arg Arg Tyr Lys Glu Asn Asn Lys Arg Ala Lys  
 325 330 335  
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 Glu Gly Ser Pro Pro Thr Tyr Arg Thr Asn Gln Gln Val Pro Pro Pro  
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 <212> DNA  
 <213> Rat

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<211> 1183

<212> DNA

<213> Rat

<400> 515

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&lt;210&gt; 516

&lt;211&gt; 1858

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 516

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&lt;210&gt; 517

&lt;211&gt; 1376

&lt;212&gt; DNA

&lt;213&gt; Rat

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&lt;211&gt; 1243

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 520

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&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 521

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&lt;211&gt; 980

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 524

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&lt;211&gt; 2929

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 525

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&lt;211&gt; 672

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 526

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&lt;213&gt; Rat

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&lt;212&gt; DNA

&lt;213&gt; Rat

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&lt;213&gt; Rat

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&lt;211&gt; 891

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 537

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&lt;212&gt; DNA

&lt;213&gt; Rat

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&lt;213&gt; Rat

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&lt;211&gt; 2351

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 544

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&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 545

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&lt;213&gt; Rat

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&lt;211&gt; 2198

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 557

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&lt;210&gt; 572

&lt;211&gt; 2920

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 572

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 <212> DNA  
 <213> Mouse

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 <211> 1930  
 <212> DNA  
 <213> Mouse

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&lt;210&gt; 576

&lt;211&gt; 2618

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 576

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&lt;211&gt; 1480

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 577

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&lt;210&gt; 585

&lt;211&gt; 1864

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 585

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&lt;211&gt; 1859

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 588

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&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 589

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&lt;210&gt; 590

&lt;211&gt; 2395

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 590

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 <213> Mouse

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&lt;213&gt; Mouse

&lt;400&gt; 592

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&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 593

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&lt;210&gt; 594

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 594

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 <212> DNA  
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 <213> Mouse

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&lt;210&gt; 597

&lt;211&gt; 1318

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 597

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&lt;211&gt; 2866

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 598

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&lt;210&gt; 599

&lt;211&gt; 1093

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 599

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&lt;210&gt; 600

&lt;211&gt; 1353

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 600

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&lt;210&gt; 601

&lt;211&gt; 3198

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 601

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 <211> 1003  
 <212> DNA  
 <213> Mouse

<400> 606						
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 <212> DNA  
 <213> Mouse

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&lt;210&gt; 609

&lt;211&gt; 3697

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 609

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&lt;210&gt; 611

&lt;211&gt; 1817

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 611

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&lt;210&gt; 612

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 612

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&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 613

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&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Mouse

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&lt;211&gt; 505

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 615

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&lt;211&gt; 2013

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 619

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&lt;212&gt; DNA

&lt;213&gt; Mouse

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aagttcttaa gttgggccat attttcaagt tctgtttgca tcaatccctc ttctgataaa 1020
agacaacctg gtctagaatg acactgtgct gtcaactggaa acaagtacag actatacagt 1080
gtggctatac agtgtgggag cagctgccct aggcacatgg gacgtgcgca tgcacatgca 1140
tgtacatgcy tgtaccatgt gtcagtccct cccctcatcc tgctcctctc ccacctctc 1200
aacactggac tactagccat ctctctaca tgctagttaa tataaaaaacc ctccccattg 1260
agagtttggt cagaaactat aggtgctga gttaaaactga attttgagtc acaaggaaga 1320
cggttctagt ttgaccaccc ctctaattgt acacaggata gctgttttta gttgttcaat 1380
ctaactctct gccgtattcc ccgagtctcc ttccagacct tccctgactc ccacttctct 1440
ccaggcatcg tggagtcca ccaatggaca gcagaggacc ctgattgtct ctgaactggc 1500
tgtcctaata ccagcagaga ccgcccagg gagccatgag gggaccccag tcaagcacca 1560
tgtcatcagc tgctgagggt ctcaatctat gcttgggtcc catgggagca ggcattgagg 1620
tcttttgctt gagagcatgc tggaaaacaa tggctctgtg agccagtcag ttatctaaat 1680
ctgcgcctca gctcttctg cccctggctg tgccacactc tcgggggtgc agaactctga 1740
gtgatcaatg agctgaatga ccagggtccaa acacctgagt ctactccgtg ctccagcact 1800
gtgaggagca gagccagcat agactgtgtt tggctgcgct ccacactgcc tacgtgacct 1860
acccccatca gcttttgtgt ggaacgtcca tctaacagca acgggtgctg ccaaaccggg 1920
tgctgagggt ttcaacttaa tttccagtga cttggaatag tgacgctata cgtctgttgg 1980
gacaggccct gcctccgccc tgggcattct cacttgggtt tgggttcagt ccaagcacag 2040
caaagccagc tttaattggga gacaggacac ggcacatgtc tgtagtccaa actaccagg 2100
aggctgaccc agaaggatca tttgactcca ctgagttcaa gacccacaga gacaacatgg 2160
aaaaaaccaq acaacagtga tgataaacca taaaaaagac gagttctgtc accatgggtt 2220
ccaatctatt gccatcactc ctttatcccc aggcacaggtt ttacacagaga ctatt 2275

```

&lt;210&gt; 624

&lt;211&gt; 688

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 624

```

Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
1          5          10          15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
20          25          30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
35          40          45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
50          55          60
Pro Leu Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65          70          75          80
Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser Glu
85          90          95
Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln Leu
100         105         110
Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu Gly

```

	115		120		125
Asn	Ala	Val	Val	Leu	Trp
130					
Leu	His	Phe	Glu	Pro	Ser
145					
Arg	Asn	Gly	Arg	Asp	Ala
Pro	Ile	Phe	Leu	Ala	Pro
Tyr	Asn	Ala	Thr	Met	Asp
Asp	Glu	Gly	Ala	Asp	Gln
210					
Gly	Gln	Glu	His	Cys	Gln
225					
Asp	Tyr	Val	Lys	Pro	Val
Pro	Asp	His	Gly	Pro	Met
Val	Ser	Val	Pro	Phe	Trp
Pro	Asp	Leu	Val	Leu	Asp
290					
Tyr	Cys	Gln	Gln	Val	Leu
305					
Thr	Leu	Ser	Phe	Asp	Thr
Arg	Val	Ala	Val	Glu	Ala
Ser	Ala	Val	Leu	Asn	Ile
Leu	Ile	Gln	Lys	Asp	Asp
370					
Glu	Arg	Arg	Leu	His	Lys
385					
Arg	Ala	Lys	Ala	Lys	Val
Ser	Val	Phe	Leu	His	His
Ser	His	Glu	Gln	Asp	Ser
Phe	His	Leu	Lys	Tyr	Glu
450					
Leu	Ser	His	Phe	Glu	Val
465					
Gly	Ile	Gly	Pro	Pro	Phe
Phe	Phe	Pro	Ile	His	Gly
Thr	Arg	Gly	Gly	Asn	Arg
Gln	Val	Asn	Thr	Ser	Cys
530					
Ser	Thr	Pro	Thr	Glu	Glu
545					
Ser	Asn	Ser	Asp	Val	Ser

```

Asn Gln Glu Thr Ser Phe Tyr Leu Val Gly Asn Leu Trp Leu Met Ser
580 585 590
Leu Lys Ala Leu Lys Tyr Arg Ser Met Lys Ile Thr Val Asn Ala Ala
595 600 605
Leu Gln Arg Gln Phe His Ser Pro Phe Ile Phe Arg Glu Glu Asp Pro
610 615 620
Ser Arg Gln Val Thr Phe Glu Ile Ser Lys Gln Glu Asp Trp Gln Val
625 630 635 640
Pro Ile Trp Ile Ile Val Gly Ser Ser Leu Gly Gly Leu Leu Leu Leu
645 650 655
Ala Leu Leu Val Leu Ala Leu Trp Lys Leu Gly Phe Phe Lys Ser Ala
660 665 670
Lys Arg Lys Arg Glu Pro Ser Leu Gly Pro Val Pro Lys Glu Leu Glu
675 680 685

```

```

<210> 625
<211> 242
<212> PRT
<213> Rat

```

```

<400> 625
Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
1 5 10 15
Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
20 25 30
Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
35 40 45
Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys
50 55 60
Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
65 70 75 80
Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
85 90 95
Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg Cys Lys
100 105 110
Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
115 120 125
Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
130 135 140
Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
145 150 155 160
Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
165 170 175
Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
180 185 190
Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
195 200 205
Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
210 215 220
Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
225 230 235 240
Gly Arg

```

```

<210> 626
<211> 576
<212> PRT

```

&lt;213&gt; Rat

&lt;400&gt; 626

```

Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Val Cys Val Leu Leu
 1          5          10          15
Pro Leu His His Gly Ala Pro Gly Pro Glu Gly Thr Ala Pro Asp Pro
 20          25          30
Ala His Tyr Arg Glu Arg Val Lys Ala Met Phe Tyr His Ala Tyr Asp
 35          40          45
Ser Tyr Leu Glu Asn Ala Phe Pro Tyr Asp Glu Leu Arg Pro Leu Thr
 50          55          60
Cys Asp Gly His Asp Thr Trp Gly Ser Phe Ser Leu Thr Leu Ile Asp
 65          70          75          80
Ala Leu Asp Thr Leu Leu Ile Leu Gly Asn Thr Ser Glu Phe Gln Arg
 85          90          95
Val Val Glu Val Leu Gln Asp Asn Val Asp Phe Asp Ile Asp Val Asn
100          105          110
Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu Ser
115          120          125
Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala Gly Trp
130          135          140
Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala Ala Arg Lys
145          150          155          160
Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro Tyr Gly Thr Val
165          170          175
Asn Leu Leu His Gly Val Asn Pro Gly Glu Thr Pro Val Thr Cys Thr
180          185          190
Ala Gly Ile Gly Thr Phe Ile Val Glu Phe Ala Thr Leu Ser Ser Leu
195          200          205
Thr Gly Asp Pro Val Phe Glu Asp Val Ala Arg Val Ala Leu Met Arg
210          215          220
Leu Trp Glu Ser Arg Ser Asp Ile Gly Leu Val Gly Asn His Ile Asp
225          230          235          240
Val Leu Thr Gly Lys Trp Val Ala Gln Asp Ala Gly Ile Gly Ala Gly
245          250          255
Val Asp Ser Tyr Phe Glu Tyr Leu Val Lys Gly Ala Ile Leu Leu Gln
260          265          270
Asp Lys Lys Leu Met Ala Met Phe Leu Glu Tyr Asn Lys Ala Ile Arg
275          280          285
Asn Tyr Thr His Phe Asp Asp Trp Tyr Leu Trp Val Gln Met Tyr Lys
290          295          300
Gly Thr Val Ser Met Pro Val Phe Gln Ser Leu Glu Ala Tyr Trp Pro
305          310          315          320
Gly Leu Gln Ser Leu Ile Gly Asp Ile Asp Asn Ala Met Arg Thr Phe
325          330          335
Leu Asn Tyr Tyr Thr Val Trp Lys Gln Phe Gly Gly Leu Pro Glu Phe
340          345          350
Tyr Asn Ile Pro Gln Gly Tyr Thr Val Glu Lys Arg Glu Gly Tyr Pro
355          360          365
Leu Arg Pro Glu Leu Ile Glu Ser Ala Met Tyr Leu Tyr Arg Ala Thr
370          375          380
Gly Asp Pro Thr Leu Leu Glu Leu Gly Arg Asp Ala Val Glu Ser Ile
385          390          395          400
Glu Lys Ile Ser Lys Val Glu Cys Gly Phe Ala Thr Ile Lys Asp Leu
405          410          415
Arg Asp His Lys Leu Asp Asn Arg Met Glu Ser Phe Phe Leu Ala Glu
420          425          430

```

```

Thr Val Lys Tyr Leu Tyr Leu Leu Phe His Pro Asn Asn Phe Ile His
      435      440      445
Asn Asn Gly Ser Thr Phe Asp Ser Val Met Thr Pro His Gly Glu Cys
      450      455      460
Ile Leu Gly Ala Gly Gly Tyr Ile Phe Asn Thr Glu Ala His Pro Ile
465      470      475      480
Asp Pro Ala Ala Leu His Cys Cys Arg Arg Leu Lys Glu Glu Gln Trp
      485      490      495
Glu Val Glu Asp Leu Ile Lys Glu Phe Tyr Ser Leu Arg Gln Ser Arg
      500      505      510
Ser Arg Ala Gln Arg Lys Thr Val Ser Ser Gly Pro Trp Glu Pro Pro
      515      520      525
Ala Gly Pro Gly Thr Leu Ser Ser Pro Glu Asn Gln Pro Arg Glu Lys
      530      535      540
Gln Pro Ala Arg Gln Arg Ala Pro Leu Leu Ser Cys Pro Ser Gln Pro
545      550      555      560
Phe Thr Ser Lys Leu Ala Leu Leu Gly Gln Val Phe Leu Asp Ser Ser
      565      570      575

```

&lt;210&gt; 627

&lt;211&gt; 226

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 627

```

Arg Lys Ile Lys Asn Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys
 1      5      10      15
Lys Glu Tyr Val Glu Cys Leu Glu Lys Lys Val Glu Thr Tyr Thr Ser
      20      25      30
Glu Asn Asn Glu Leu Trp Lys Lys Val Glu Thr Leu Glu Thr Ala Asn
      35      40      45
Arg Thr Leu Leu Gln Gln Leu Gln Lys Leu Gln Thr Leu Val Thr Ser
      50      55      60
Lys Ile Ser Arg Pro Tyr Lys Met Ala Ala Thr Gln Thr Gly Thr Cys
65      70      75      80
Leu Met Val Ala Ala Leu Cys Phe Val Leu Val Leu Gly Ser Leu Ala
      85      90      95
Pro Cys Leu Pro Ala Phe Ser Ser Gly Ser Lys Thr Val Lys Glu Asp
      100      105      110
Pro Val Ala Ala Asp Ser Val Tyr Ala Ala Ser Gln Met Pro Ser Arg
      115      120      125
Ser Leu Leu Phe Tyr Asp Asp Gly Ala Gly Ser Trp Glu Asp Gly His
      130      135      140
Arg Gly Ala Leu Leu Pro Val Glu Pro Pro Glu Gly Trp Glu Leu Lys
145      150      155      160
Pro Gly Gly Pro Ala Glu Pro Arg Pro Gln Asp His Leu Arg His Asp
      165      170      175
His Ala Asp Ser Ile His Glu Thr Thr Lys Tyr Leu Arg Glu Thr Trp
      180      185      190
Pro Glu Asp Thr Glu Asp Asn Gly Ala Ser Pro Asn Phe Ser His Pro
      195      200      205
Lys Glu Trp Phe His Asp Arg Asp Leu Gly Pro Asn Thr Thr Ile Lys
210      215      220
Leu Ser
225

```

&lt;210&gt; 628

<211> 82  
 <212> PRT  
 <213> Rat

<400> 628  
 Pro Ile Thr Leu Ser Cys Gln Ser Gly Asn Ala Ala Ser Leu Gln Pro  
 1 5 10 15  
 Leu His Phe Pro Pro Val Pro Pro Glu Ala Cys Pro Cys Ala Phe Arg  
 20 25 30  
 Leu Arg Pro Phe Cys Leu His Thr Gly Cys Ala Gly Cys Ser Leu Arg  
 35 40 45  
 Ala Ala Thr Glu Gln Cys Ala Val Ala Leu Ala Pro Gln Leu Pro Ser  
 50 55 60  
 Ala Ser Arg Ala Phe Pro Pro Leu Thr Leu Cys Asn Pro Cys Val Leu  
 65 70 75 80  
 Thr Arg

<210> 629  
 <211> 242  
 <212> PRT  
 <213> Rat

<400> 629  
 Met Ala Gly Ala Gly Pro Val Leu Ser Ile Leu Gly Leu Leu Leu Val  
 1 5 10 15  
 Ser Ala Leu Phe Gly Val Leu Gly Glu Arg Pro Asn Pro Asp Leu Gly  
 20 25 30  
 Ala His Pro Glu Arg Arg Ser Gln Val Gly Pro Gly Ala Thr Glu Pro  
 35 40 45  
 Arg Arg Gln Pro Pro Pro Lys Asp Gln Arg Glu Arg Ala Arg Ala Gly  
 50 55 60  
 Ser Leu Ser Leu Gly Ala Leu Tyr Thr Ala Ala Ile Val Ala Phe Val  
 65 70 75 80  
 Leu Phe Lys Cys Leu Gln Gln Gly Pro Asp Glu Ala Ala Val Pro Arg  
 85 90 95  
 Glu Glu Lys Asn Lys Lys Lys Ser Ser Gln Ser Glu Gln Gln Leu Val  
 100 105 110  
 Gln Leu Thr Gln Gln Leu Ala Gln Thr Glu Glu His Leu Asn Asn Leu  
 115 120 125  
 Met Thr Gln Leu Asp Pro Leu Phe Glu Arg Val Thr Thr Leu Val Gly  
 130 135 140  
 Thr Gln Arg Glu Leu Leu Asn Ala Lys Leu Lys Thr Ile His His Leu  
 145 150 155 160  
 Leu Gln Asp Cys Lys Pro Gly Ile Gly Val Glu Ala Pro Glu Pro Glu  
 165 170 175  
 Ala Pro Ile His Phe Pro Glu Asp Leu Gly Lys Glu Asp Gln Glu Asp  
 180 185 190  
 Ala Gly Asn Ser Gln Ala Trp Glu Glu Pro Ile Asn Trp Ser Ser Glu  
 195 200 205  
 Thr Trp Asn Leu Ala Pro Ser Trp Glu Val Glu Gln Gly Leu Arg Arg  
 210 215 220  
 Arg Trp His Lys Thr Lys Gly Pro Ala Val Asn Gly Gly Gln Ala Leu  
 225 230 235 240  
 Lys Val

<210> 630  
 <211> 289  
 <212> PRT  
 <213> Rat

<400> 630  
 Met Ile Val Leu Leu Tyr Val Thr Ser Leu Ala Ile Cys Ala Ser Gly  
 1 5 10 15  
 Gln Pro Arg Gly Asn Gln Ala Lys Gly Glu Ser Tyr Ser Pro Arg Tyr  
 20 25 30  
 Ile Cys Ser Ile Pro Gly Leu Pro Gly Pro Pro Gly Pro Gly Ala  
 35 40 45  
 Asn Gly Ser Pro Gly Pro His Gly Arg Ile Gly Leu Pro Gly Arg Asp  
 50 55 60  
 Gly Arg Asp Gly Arg Lys Gly Glu Lys Gly Glu Lys Gly Thr Ala Gly  
 65 70 75 80  
 Leu Lys Gly Lys Thr Gly Pro Leu Gly Leu Ala Gly Glu Lys Gly Asp  
 85 90 95  
 Gln Gly Glu Thr Gly Lys Lys Gly Pro Ile Gly Pro Glu Gly Glu Lys  
 100 105 110  
 Gly Glu Val Gly Pro Ala Gly Pro Gly Pro Lys Gly Asp Arg Gly  
 115 120 125  
 Asp Gln Gly Asp Pro Gly Leu Pro Gly Val Cys Arg Cys Gly Ser Ile  
 130 135 140  
 Val Leu Lys Ser Ala Phe Ser Val Gly Ile Thr Thr Ser Tyr Pro Glu  
 145 150 155 160  
 Glu Arg Leu Pro Ile Ile Phe Asn Lys Val Leu Phe Asn Glu Gly Glu  
 165 170 175  
 His Tyr Asn Pro Ala Thr Gly Lys Phe Ile Cys Ala Phe Pro Gly Ile  
 180 185 190  
 Tyr Tyr Phe Ser Tyr Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile  
 195 200 205  
 Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn  
 210 215 220  
 Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Val Ile Tyr Leu Gln  
 225 230 235 240  
 Pro Glu Asp Glu Val Trp Leu Glu Ile Phe Phe Asn Asp Gln Asn Gly  
 245 250 255  
 Leu Phe Ser Asp Pro Gly Trp Ala Asp Ser Leu Phe Ser Gly Phe Leu  
 260 265 270  
 Leu Tyr Val Asp Thr Asp Tyr Leu Asp Ser Ile Ser Glu Asp Asp Glu  
 275 280 285  
 Leu

<210> 631  
 <211> 213  
 <212> PRT  
 <213> Rat

<400> 631  
 Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln  
 1 5 10 15  
 Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg  
 20 25 30  
 Ser His Ser Phe Asn Ala Thr Ala Glu Leu Asp Leu Thr Pro Ser Gly  
 35 40 45



```

Ala Ala His Leu Glu Gly Pro Ala Ala Ser Ser Trp Glu Tyr Ser Asp
 50      55      60
Pro Asn Ser Pro Val Ile Leu Cys Ser Tyr Leu Pro Asp Glu Phe Val
 65      70      75      80
Asp Cys Asp Ala Pro Val Asp His Val Gly Asn Ala Thr Ala Tyr Gln
      85      90      95
Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly Gly Gln Ala Tyr Ser Asp
      100      105      110
Val Glu His Thr Ala Val Gln Cys Arg Ala Leu Glu Gly Ile Glu Cys
      115      120      125
Ala Ser Pro Arg Thr Phe Leu Arg Lys Asn Lys Pro Cys Ile Lys Tyr
      130      135      140
Thr Gly His Tyr Phe Ile Thr Thr Leu Leu Tyr Ser Phe Phe Leu Gly
      145      150      155      160
Cys Phe Gly Val Asp Arg Phe Cys Leu Gly His Thr Gly Thr Ala Val
      165      170      175
Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly Ile Trp Trp Phe Val Asp
      180      185      190
Leu Ile Leu Leu Ile Thr Gly Gly Leu Met Pro Ser Asp Gly Ser Asn
      195      200      205
Trp Cys Thr Val Tyr
      210

```

```

<210> 632
<211> 167
<212> PRT
<213> Rat

```

```

<400> 632
Met Ala Ser Pro Arg Thr Ile Thr Ile Val Ala Leu Ser Val Ala Leu
 1      5      10      15
Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu
      20      25      30
Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr Val
      35      40      45
Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
      50      55      60
Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
      65      70      75      80
Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
      85      90      95
Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
      100      105      110
Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg
      115      120      125
Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Phe Glu Lys Lys Ala
      130      135      140
Leu Pro Glu Ser Ala Glu Glu Gln Pro Ser Leu Tyr Glu Lys Ala Pro
      145      150      155      160
Gln Gly Lys Val Lys Val Ser
      165

```

```

<210> 633
<211> 138
<212> PRT
<213> Rat

```

&lt;400&gt; 633

```

Phe Ile Arg Gly Met Leu Lys Leu Ile Leu Leu Leu Phe Ser Gly
 1           5           10           15
Ala Thr Leu Ser Ser Thr Trp Phe Thr Leu Thr Cys Leu Asn Ser Val
           20           25           30
Thr His Leu Pro Leu Thr Thr Val Thr Leu Tyr Ala Ser Cys Ile Leu
           35           40           45
Leu Gly Val Phe Leu Asn Ser Ser Val Pro Ile Phe Phe Glu Leu Phe
 50           55           60
Val Glu Thr Val Tyr Pro Val Pro Glu Gly Ile Thr Cys Gly Val Val
 65           70           75           80
Thr Phe Leu Ser Asn Met Phe Met Gly Val Leu Leu Phe Phe Val Thr
           85           90           95
Phe Tyr His Thr Glu Leu Ser Trp Phe Asn Trp Cys Leu Pro Gly Ser
           100          105          110
Cys Leu Leu Ser Leu Leu Leu Ile Leu Cys Phe Arg Glu Ser Tyr Asp
          115          120          125
Arg Leu Tyr Leu Asp Val Val Val Ser Val
          130          135

```

&lt;210&gt; 634

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 634

```

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
 1           5           10           15
Ala Val Leu Asn Phe Lys Leu Lys Lys Asp Thr Gln Gly Phe Gly
           20           25           30
Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
           35           40           45
Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Val Phe
 50           55           60
Met Met Leu Cys Met Ile Val Leu Phe Gly Ser
 65           70           75

```

&lt;210&gt; 635

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 635

```

Met Val Ala Ala Val Ala Thr Ala Trp Leu Leu Leu Trp Ala Ala Ala
 1           5           10           15
Cys Thr Gln Ser Glu Gln Asp Phe Tyr Asp Phe Lys Ala Val Asn Ile
           20           25           30
Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly Ser Val Ser Leu
           35           40           45
Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr Asp Gln Asn Tyr Arg
 50           55           60
Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly Pro Tyr His Phe Asn Val
 65           70           75           80
Leu Ala Phe Pro Cys Asn Gln Phe Gly Gln Gln Glu Pro Asp Ser Asn
           85           90           95
Arg Glu Ile Glu Asn Phe Ala Arg Arg Thr Tyr Ser Val Ser Phe Pro
          100          105          110

```

```

Met Phe Ser Lys Ile Ala Val Thr Gly Thr Gly Ala His Pro Ala Phe
    115      120      125
Lys Tyr Leu Thr Gln Thr Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp
    130      135      140
Lys Tyr Leu Val Ala Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro
    145      150      155      160
Thr Val Pro Val Glu Glu Ile Lys Pro Arg Ile Thr Glu Gln Val Met
    165      170      175
Lys Leu Ile Leu Gln Lys Arg Glu Asp Leu
    180      185

```

&lt;210&gt; 636

&lt;211&gt; 930

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 636

```

Met Pro Ser Leu Leu Ser Leu Val Leu Thr Phe Leu Ala Val Ser Ser
  1      5      10      15
Pro Ser Cys Cys Gln Asn Ser Asp Thr Ala Ser Pro Lys Ala Ser Asn
    20      25      30
Gly Ala Ser Phe Leu Trp Asn Asn Met Arg Leu Pro Glu Tyr Ile Thr
    35      40      45
Pro Ile His Tyr Asp Leu Met Ile His Ala Asn Leu Ser Thr Leu Thr
    50      55      60
Phe Trp Gly Lys Thr Glu Val Glu Ile Thr Val Ser Gln Pro Thr Ser
    65      70      75      80
Thr Ile Ile Met His Ser His Gln Leu Gln Ile Ser Lys Ala Thr Leu
    85      90      95
Arg Arg Gly Ala Glu Glu Met Leu Pro Glu Glu Pro Leu Lys Leu Met
    100      105      110
Glu Tyr Ser Ala His Glu Gln Val Ala Leu Leu Thr Ala Gln Pro Leu
    115      120      125
Leu Ala Gly Ser Val Tyr Thr Val Ile Ile Thr Tyr Ala Ala Asn Leu
    130      135      140
Ser Glu Asn Phe His Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Gln Glu
    145      150      155      160
Gly Glu Arg Arg Ile Leu Ala Ala Thr Gln Phe Glu Pro Thr Ala Ala
    165      170      175
Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Ala Leu Lys Ala Ser Phe
    180      185      190
Ser Ile Lys Ile Lys Arg Asp Pro Arg His Leu Ala Ile Ser Asn Met
    195      200      205
Pro Leu Val Lys Ser Val Thr Val Ala Glu Gly Leu Ile Glu Asp His
    210      215      220
Phe Asp Ile Thr Val Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile
    225      230      235      240
Ser Asp Phe Lys Ser Val Ser Lys Met Thr Lys Ser Gly Val Lys Val
    245      250      255
Ser Val Tyr Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu
    260      265      270
Asp Ala Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile
    275      280      285
Pro Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln
    290      295      300
Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser Ala
    305      310      315      320

```

Leu Leu Tyr Asp Lys Glu Lys Ser Ser Ala Ser Ser Lys Leu Gly Ile  
 325 330 335  
 Thr Met Thr Val Ser His Glu Leu Ala His Gln Trp Phe Gly Asn Leu  
 340 345 350  
 Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala  
 355 360 365  
 Lys Phe Met Glu Phe Val Ser Val Thr Val Thr His Pro Glu Leu Lys  
 370 375 380  
 Val Glu Glu Tyr Phe Phe Gly Lys Cys Val Asn Ala Met Glu Val Asp  
 385 390 395 400  
 Ala Leu Asn Ser Ser His Pro Val Ser Thr Pro Val Glu Asn Pro Ala  
 405 410 415  
 Gln Ile Arg Glu Met Phe Asp Glu Val Ser Tyr Glu Lys Gly Ala Cys  
 420 425 430  
 Ile Leu Asn Met Leu Arg Asp Tyr Leu Ser Ala Asp Thr Phe Lys Arg  
 435 440 445  
 Gly Ile Val Gln Tyr Leu Gln Lys Tyr Ser Tyr Lys Asn Thr Lys Asn  
 450 455 460  
 Glu Asp Leu Trp Asn Ser Met Met His Ile Cys Pro Thr Asp Gly Thr  
 465 470 475 480  
 Gln Thr Met Asp Gly Phe Cys Ser Arg Asn Gln His Ser Ser Ser Thr  
 485 490 495  
 Ser His Trp Arg Gln Glu Val Ile Asp Ile Lys Ser Met Met Asn Thr  
 500 505 510  
 Trp Thr Leu Gln Lys Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly  
 515 520 525  
 Arg Asn Val His Leu Lys Gln Glu His Tyr Met Lys Gly Ser Glu Cys  
 530 535 540  
 Phe Pro Glu Thr Gly Ser Leu Trp His Val Pro Leu Thr Phe Ile Thr  
 545 550 555 560  
 Ser Lys Ser Asp Ser Val Gln Arg Phe Leu Leu Lys Thr Lys Thr Asp  
 565 570 575  
 Val Ile Ile Leu Pro Glu Ala Val Glu Trp Ile Lys Phe Asn Val Gly  
 580 585 590  
 Met Asn Gly Tyr Tyr Ile Val His Tyr Gly Asp Asp Gly Trp Ala Ser  
 595 600 605  
 Leu Asn Gly Leu Leu Lys Glu Ala His Thr Thr Ile Ser Ser Asn Asp  
 610 615 620  
 Arg Ala Ser Leu Ile Asn Asn Ala Phe Gln Leu Val Ser Ile Gly Lys  
 625 630 635 640  
 Leu Ser Ile Glu Lys Ala Leu Asp Leu Ile Leu Tyr Leu Lys Asn Glu  
 645 650 655  
 Thr Glu Ile Met Pro Ile Phe Gln Gly Leu Asn Glu Leu Ile Pro Met  
 660 665 670  
 Tyr Lys Leu Met Glu Lys Arg Asp Met Val Glu Val Glu Thr Gln Phe  
 675 680 685  
 Lys Asp Phe Leu Leu Arg Leu Leu Lys Asp Leu Ile Asn Lys Gln Thr  
 690 695 700  
 Trp Thr Asp Glu Gly Ser Val Ser Glu Arg Met Leu Arg Ser Gln Leu  
 705 710 715 720  
 Leu Leu Leu Ala Cys Val His Arg Tyr Gln Leu Cys Val Gln Arg Ala  
 725 730 735  
 Glu Arg Tyr Phe Arg Glu Trp Lys Ala Ser Asn Gly Asn Met Ser Leu  
 740 745 750  
 Pro Ile Asp Val Thr Leu Ala Val Phe Ala Val Gly Ala Gln Asn Thr  
 755 760 765  
 Glu Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Ser Ser Leu Ser Ser

```

      770      775      780
Thr Glu Lys Ser Gln Ile Glu Phe Ser Leu Cys Ile Ser Gln Asp Pro
785      790      795      800
Glu Lys Leu Gln Trp Leu Leu Asp Gln Ser Phe Lys Gly Glu Ile Ile
      805      810      815
Lys Thr Gln Glu Phe Pro His Ile Leu Thr Leu Ile Gly Arg Asn Pro
      820      825      830
Val Gly Tyr Pro Leu Ala Trp Lys Phe Leu Lys Glu Asn Trp Asn Lys
      835      840      845
Ile Val Gln Lys Phe Glu Leu Gly Ser Ser Ser Ile Ala His Met Val
      850      855      860
Met Gly Thr Thr Asn Gln Phe Ser Thr Arg Ala Arg Leu Glu Glu Val
      865      870      875      880
Lys Gly Phe Phe Ser Ser Leu Lys Lys Asn Gly Ser Gln Leu Arg Cys
      885      890      895
Val Gln Gln Thr Ile Glu Thr Ile Glu Glu Asn Ile Arg Trp Met Asp
      900      905      910
Lys Asn Phe Asp Lys Ile Arg Leu Trp Leu Gln Lys Glu Arg Gln Glu
      915      920      925
Leu Leu
      930

```

<210> 637  
 <211> 161  
 <212> PRT  
 <213> Rat

```

<400> 637
Met Ala Tyr His Ser Gly Tyr Gly Val His Ala Met Ala Phe Ile Thr
1      5      10      15
Tyr Val Leu Leu Ala Gly Met Ala Leu Gly Ile Gln Gln Arg Phe Ser
      20      25      30
Pro Glu Val Leu Gly Leu Cys Ala Ser Thr Ala Leu Val Trp Val Leu
      35      40      45
Met Glu Val Leu Ala Leu Leu Leu Gly Leu Tyr Leu Ala Thr Val Arg
      50      55      60
Ser Glu Leu Gly Thr Phe His Leu Leu Ala Tyr Ser Gly Tyr Lys Tyr
65      70      75      80
Val Gly Met Ile Leu Ser Val Leu Thr Gly Leu Leu Phe Gly Ser Asp
      85      90      95
Gly Tyr Tyr Val Ala Leu Ala Trp Thr Ser Ser Ala Leu Met Tyr Phe
      100      105      110
Thr Val Arg Ser Leu Arg Thr Ala Ala Ser Gly Pro Asp Ser Met Gly
      115      120      125
Gly Pro Thr Pro Arg Gln His Leu Gln Leu Tyr Leu Thr Leu Gly Ala
      130      135      140
Ala Ala Phe Gln Pro Leu Ile Ile Tyr Trp Leu Thr Phe His Leu Val
145      150      155      160
Arg

```

<210> 638  
 <211> 165  
 <212> PRT  
 <213> Rat

<400> 638

```

Met Ala Arg Ala Ala Gly Ile Thr Ala Ala Ile Thr Leu Ala Leu Leu
 1          5          10          15
Gly Val Leu Ala Leu Gly Ala Gly Asp Gly Asp Phe Arg Leu Asp Asp
          20          25          30
Ala Leu Glu Asp Thr Asp Lys Lys Pro Thr Pro Lys Pro Pro Thr Pro
          35          40          45
Lys Lys Pro Ser Ser Gly Asp Phe Asp Leu Glu Glu Ala Leu Thr Gly
 50          55          60
Gly Ala Asp Glu Asp Pro Arg Arg Pro Gly Ser Arg Pro Lys Pro Asp
 65          70          75          80
Pro Lys Pro Pro Gly Pro Pro Arg Asp Ser Gly Gly Ile Ser Asp Arg
          85          90          95
Asp Leu Glu Asp Val Ala Gly His Gly Gly Arg Gly Gly Gly Ala Gly
          100          105          110
Asp Arg Gly Thr Asp Gly Ala Glu Ser Glu Gly Gln Pro Gln Gly Leu
          115          120          125
Ile Pro Gly Val Val Ala Ala Val Leu Ala Ala Leu Ala Gly Ala Val
          130          135          140
Ser Ser Phe Val Ala Tyr Gln Lys Arg Arg Leu Cys Phe Arg Glu Gly
145          150          155          160
Gly Ser Ala Pro Val
          165

```

<210> 639  
 <211> 61  
 <212> PRT  
 <213> Rat

```

<400> 639
Met His Ile Tyr Lys Tyr Val His Ile Asn Tyr Tyr Leu His Leu His
 1          5          10          15
Ile Cys Ile Tyr Val Tyr Thr His Ile Ser Val Gly Met Cys Ile Arg
          20          25          30
Ile Cys Leu Pro Ser Ser Ser His Trp Lys Lys Glu Ser Ile Arg Ser
          35          40          45
Gly Gly Ser Lys Asn Ala His Tyr Pro Gly Ser Gly Ile
 50          55          60

```

<210> 640  
 <211> 73  
 <212> PRT  
 <213> Rat

```

<400> 640
Met Cys Phe Ser Leu Cys Ser Val Glu Val Phe Phe Leu Lys Gln Asn
 1          5          10          15
Ser Asn Leu Leu Pro Ala His Ile Phe Ile Arg Ala Ser Pro Ile Cys
          20          25          30
Ile Ile Gly Asn Glu Tyr Glu Tyr Ile Phe Met Tyr Val Cys Asn His
          35          40          45
Arg Ser His Leu Tyr Leu Gly Phe Ala Ala Ala Asp Tyr Phe Phe Pro
 50          55          60
His His Gly Thr Gly Asn Cys Phe Gln
 65          70

```

<210> 641

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 641

```

Met Pro Val Leu Trp Leu Leu Leu Leu Leu Pro Leu Leu Pro Leu Leu
 1          5          10          15
Ala Met Leu Cys Gln Gln Arg Ser Pro Gly Ala Arg Pro Cys Trp Leu
          20          25          30
Ile Ser Leu Gln His Arg Val Ala Cys Val Val Leu Ser Trp Ala Ala
          35          40          45
Ala Trp Gln Arg Arg Lys Leu Glu Gln Ser Thr Leu Asn Val Ser Gln
          50          55          60
Ser Gln Gln Gln Ala Leu Met Gly Cys Leu Lys Glu Ala Gln Gly Ser
65          70          75          80
Cys Cys Leu Pro Arg Glu Asn Thr Asp Met Thr Thr Phe Arg Asn Leu
          85          90          95
Pro Leu Thr Lys Thr Ser His Thr Gln Lys Glu Ser Glu Glu Lys
          100          105          110
Leu Leu Pro Pro Thr Leu Pro Gln Tyr His Gly Asp Ala Ser Leu Gln
          115          120          125
Val Thr Leu Leu Gly Leu Met Thr Leu Asn Lys Ala Tyr Pro Glu Val
          130          135          140
Leu Ala Pro Gly Ser Thr Ala Cys Val Thr Pro Thr Ser Pro Trp Pro
145          150          155          160
Tyr Ser Val Pro Trp Leu Gly His Ala Leu Gly Arg Val Ser Pro Ile
          165          170          175
Gly Ala Lys Asp Ala Arg Thr Leu Leu Leu Glu Ala Leu Ile Ser Pro
          180          185          190
Gly Leu Arg Val Leu Glu Ala Arg Thr Ala Val Glu Leu Leu Asp Val
          195          200          205
Phe Val Gly Leu Glu Ala Asp Gly Glu Glu Leu Ala Glu Val Ile Ala
210          215          220
Ser Gly Ser Leu Gly Lys Leu Pro Arg Arg Ala Ala Glu Leu Gln Glu
225          230          235          240
Ala Leu Glu Gln Gly Pro Arg Gly Leu Ala Leu Arg Leu Trp Pro Lys
          245          250          255
Leu Gln Val Val Val Thr Leu Asp Ala Gly Gly Gln Ala Glu Ala Val
          260          265          270
Ala Ala Leu Arg Val Leu Trp Cys Gln Gly Leu Ala Phe Phe Ser Pro
          275          280          285
Ala Tyr Ala Ala Ser Gly Gly Val Met Ala Ile Asn Leu Trp Pro Glu
290          295          300
Gln Pro Gln Gly Ser Tyr Leu Leu Ser Pro Gly Val Pro Phe Ile Glu
305          310          315          320
Leu Leu Pro Ile Lys Glu Gly Thr Gln Glu Glu Ala Ala Ser Thr Leu
          325          330          335
Leu Leu Thr Asp Val Arg Arg Glu Glu Lys Tyr Glu Leu Val Leu Thr
          340          345          350
Asp Ser Thr Ser Leu Thr Arg Cys Arg Leu Gly Asp Val Val Gln Val
          355          360          365
Ile Gly Thr Tyr Asn Gln Cys Pro Val Val Arg Phe Thr Cys Arg Leu
370          375          380
Gly Gln Thr Leu Ser Val Arg Gly Glu Val Thr Asp Glu Asn Val Phe
385          390          395          400
Ser Val Ala Leu Ala Gln Ala Val Gly Gln Cys Gln Gly Pro Ser Cys
          405          410          415

```

Trp Thr Met Ser Val Trp Arg Ala Thr Phe Trp Thr Pro Met Arg Asp  
 420 425 430  
 Pro Pro His Thr Thr Lys Cys Leu Trp Ser  
 435 440

<210> 642  
 <211> 65  
 <212> PRT  
 <213> Rat

<400> 642  
 Met Thr Val Cys Thr Leu Leu Val Ala Lys Ser Thr Leu Leu Leu Ser  
 1 5 10 15  
 Leu Ser Cys Leu Leu Cys Ser Leu Phe Leu Tyr Ser Val Ser Gly  
 20 25 30  
 Ser Tyr Ser Arg Cys Pro Val Arg Trp Leu Val Cys Leu Ser Ser Gln  
 35 40 45  
 Leu Pro Trp Ala Thr Ser Gln Ser Leu Leu Lys Arg Lys Leu Ser Met  
 50 55 60  
 Asn  
 65

<210> 643  
 <211> 197  
 <212> PRT  
 <213> Rat

<400> 643  
 Pro Arg Pro Gly Arg Ala Arg Thr Leu Arg Ser Pro Ser Gly Ser Arg  
 1 5 10 15  
 Val Val Gln Arg Pro Arg Asn Asp Gly Val Ala Ala Leu Thr Gly Ala  
 20 25 30  
 Gly Gly Cys Arg Ala Pro Arg Ala Gly Met Ala Gly Gln Phe Arg Ser  
 35 40 45  
 Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln Ile Val Leu Met Gln  
 50 55 60  
 Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp Ala  
 65 70 75 80  
 Leu Val Arg Ser Asn Pro Ser Leu Asp Gln Met Phe Asp Ala Glu Ile  
 85 90 95  
 Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe Val  
 100 105 110  
 Leu Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg Arg  
 115 120 125  
 Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His Leu  
 130 135 140  
 Leu Gly Cys Trp Leu Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr Trp  
 145 150 155 160  
 Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly Glu  
 165 170 175  
 Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Ser Ser Ala  
 180 185 190  
 Pro Lys Ser Asn Val  
 195

<210> 644  
 <211> 930



&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 644

```

Met Pro Ser Leu Leu Ser Leu Val Leu Thr Phe Leu Ala Val Ser Ser
 1      5      10      15
Pro Ser Cys Cys Gln Asn Ser Asp Thr Ala Ser Pro Lys Ala Ser Asn
 20      25      30
Gly Ala Ser Phe Leu Trp Asn Asn Met Arg Leu Pro Glu Tyr Ile Thr
 35      40      45
Pro Ile His Tyr Asp Leu Met Ile His Ala Asn Leu Ser Thr Leu Thr
 50      55      60
Phe Trp Gly Lys Thr Glu Val Glu Ile Thr Val Ser Gln Pro Thr Ser
 65      70      75      80
Thr Ile Ile Met His Ser His Gln Leu Gln Ile Ser Lys Ala Thr Leu
 85      90      95
Arg Arg Gly Ala Glu Glu Met Leu Pro Glu Glu Pro Leu Lys Leu Met
 100     105     110
Glu Tyr Ser Ala His Glu Gln Val Ala Leu Leu Thr Ala Gln Pro Leu
 115     120     125
Leu Ala Gly Ser Val Tyr Thr Val Ile Ile Thr Tyr Ala Ala Asn Leu
 130     135     140
Ser Glu Asn Phe His Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Gln Glu
 145     150     155     160
Gly Glu Arg Arg Ile Leu Ala Ala Thr Gln Phe Glu Pro Thr Ala Ala
 165     170     175
Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Ala Leu Lys Ala Ser Phe
 180     185     190
Ser Ile Lys Ile Lys Arg Asp Pro Arg His Leu Ala Ile Ser Asn Met
 195     200     205
Pro Leu Val Lys Ser Val Thr Val Ala Glu Gly Leu Ile Glu Asp His
 210     215     220
Phe Asp Ile Thr Val Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile
 225     230     235     240
Ser Asp Phe Lys Ser Val Ser Lys Met Thr Lys Ser Gly Val Lys Val
 245     250     255
Ser Val Tyr Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu
 260     265     270
Asp Ala Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile
 275     280     285
Pro Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln
 290     295     300
Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser Ala
 305     310     315     320
Leu Leu Tyr Asp Lys Glu Lys Ser Ser Ala Ser Ser Lys Leu Gly Ile
 325     330     335
Thr Met Thr Val Ser His Glu Leu Ala His Gln Trp Phe Gly Asn Leu
 340     345     350
Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala
 355     360     365
Lys Phe Met Glu Phe Val Ser Val Thr Val Thr His Pro Glu Leu Lys
 370     375     380
Val Glu Glu Tyr Phe Phe Gly Lys Cys Phe Asn Ala Met Glu Val Asp
 385     390     395     400
Ala Leu Asn Ser Ser His Pro Val Ser Thr Pro Val Glu Asn Pro Ala
 405     410     415
Gln Ile Arg Glu Met Phe Asp Glu Val Ser Tyr Glu Lys Gly Ala Cys

```

Ile	Leu	Asn	Met	Leu	Arg	Asp	Tyr	Leu	Ser	Ala	Asp	Thr	Phe	Lys	Arg
Gly	Ile	Val	Gln	Tyr	Arg	Gln	Lys	Tyr	Ser	Tyr	Lys	Asn	Thr	Lys	Asn
Glu	Asp	Leu	Trp	Asn	Ser	Met	Met	His	Ile	Cys	Pro	Thr	Asp	Gly	Thr
Gln	Thr	Met	Asp	Gly	Phe	Cys	Ser	Arg	Asn	Gln	His	Ser	Ser	Ser	Thr
Ser	His	Trp	Arg	Gln	Glu	Val	Ile	Asp	Ile	Lys	Ser	Met	Met	Asn	Thr
Trp	Thr	Leu	Gln	Lys	Gly	Phe	Pro	Leu	Ile	Thr	Ile	Thr	Val	Arg	Gly
Arg	Asn	Val	His	Leu	Lys	Gln	Glu	His	Tyr	Met	Lys	Gly	Ser	Glu	Cys
Phe	Pro	Glu	Thr	Gly	Ser	Leu	Trp	His	Val	Pro	Leu	Thr	Phe	Ile	Thr
Ser	Lys	Ser	Asp	Ser	Val	Gln	Arg	Phe	Leu	Leu	Lys	Thr	Lys	Thr	Asp
Val	Ile	Ile	Leu	Pro	Glu	Ala	Val	Glu	Trp	Ile	Lys	Phe	Asn	Val	Gly
Met	Asn	Gly	Tyr	Tyr	Ile	Val	His	Tyr	Gly	Asp	Asp	Gly	Trp	Ala	Ser
Leu	Asn	Gly	Leu	Leu	Lys	Glu	Ala	His	Thr	Thr	Ile	Ser	Ser	Asn	Asp
Arg	Ala	Ser	Leu	Ile	Asn	Asn	Ala	Phe	Gln	Leu	Val	Ser	Ile	Gly	Lys
Leu	Ser	Ile	Glu	Lys	Ala	Leu	Asp	Leu	Ile	Leu	Tyr	Leu	Lys	Asn	Glu
Thr	Glu	Ile	Met	Pro	Ile	Phe	Gln	Gly	Leu	Asn	Glu	Leu	Ile	Pro	Met
Tyr	Lys	Leu	Met	Glu	Lys	Arg	Asp	Met	Val	Glu	Val	Glu	Thr	Gln	Phe
Lys	Asp	Phe	Leu	Leu	Arg	Leu	Leu	Lys	Asp	Leu	Ile	Asn	Lys	Gln	Thr
Trp	Thr	Asp	Glu	Gly	Ser	Val	Ser	Glu	Arg	Met	Leu	Arg	Ser	Gln	Leu
Leu	Leu	Leu	Ala	Cys	Val	His	Arg	Tyr	Gln	Leu	Cys	Val	Gln	Arg	Ala
Glu	Arg	Tyr	Phe	Arg	Glu	Trp	Lys	Ala	Ser	Asn	Gly	Asn	Met	Ser	Leu
Pro	Ile	Asp	Val	Thr	Leu	Ala	Val	Phe	Ala	Val	Gly	Ala	Gln	Asn	Thr
Glu	Gly	Trp	Asp	Phe	Leu	Tyr	Ser	Lys	Tyr	Gln	Ser	Ser	Leu	Ser	Ser
Thr	Glu	Lys	Ser	Gln	Ile	Glu	Phe	Ser	Leu	Cys	Ile	Ser	Gln	Asp	Pro
Glu	Lys	Leu	Gln	Trp	Leu	Leu	Asp	Gln	Ser	Phe	Lys	Gly	Glu	Ile	Ile
Lys	Thr	Gln	Glu	Phe	Pro	His	Ile	Leu	Thr	Leu	Ile	Gly	Arg	Asn	Pro
Val	Gly	Tyr	Pro	Leu	Ala	Trp	Lys	Phe	Leu	Lys	Glu	Asn	Trp	Asn	Lys
Ile	Val	Gln	Lys	Phe	Glu	Leu	Gly	Ser	Ser	Ser	Ile	Ala	His	Met	Val
Met	Gly	Thr	Thr	Asn	Gln	Phe	Ser	Thr	Lys	Ala	Arg	Leu	Glu	Lys	Val

Lys Gly Phe Phe Ser Ser Leu Lys Lys Asn Gly Phe Gln Leu Arg Cys  
 885 890 895  
 Val Gln Gln Thr Ile Glu Thr Ile Glu Lys Asn Ile Arg Trp Met Asp  
 900 905 910  
 Lys Asn Phe Asp Lys Ile Arg Leu Trp Leu Gln Lys Lys Arg Gln Glu  
 915 920 925  
 Leu Leu  
 930

<210> 645  
 <211> 179  
 <212> PRT  
 <213> Rat

<400> 645  
 Met Leu His Asn Val Ser Lys Gly Val Val Tyr Ser Ala Thr Val Val  
 1 5 10 15  
 Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser Arg Lys  
 20 25 30  
 Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp Pro  
 35 40 45  
 Asp Arg Asp Gln Arg His Gly Asp Ser Ser Ile Phe Val Asp Ser Pro  
 50 55 60  
 His Gly Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Ala Asp Leu  
 65 70 75 80  
 Gly Cys Arg Leu Tyr Leu His Ile Pro Gln Gln Gln Glu Glu Val  
 85 90 95  
 Gln Arg Leu Leu Ile Leu Gly Glu Pro Ala Lys Gly Trp Gln Gly Leu  
 100 105 110  
 Ala Gly Gln Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala Cys  
 115 120 125  
 Asp Gln Asp Pro Ala Tyr Ala Leu Leu Arg Asp Trp Ala Ala Gln Glu  
 130 135 140  
 Gly Ser Gly Ala Thr Leu Arg Val Leu Glu Asp Ala Leu Thr Ala Ile  
 145 150 155 160  
 Gly Arg Glu Asp Val Val Gln Val Leu Ser Ser Pro Ala Glu Gly Cys  
 165 170 175  
 Ser Val Val

<210> 646  
 <211> 298  
 <212> PRT  
 <213> Rat

<400> 646  
 Met Lys Tyr Leu Leu Asp Leu Ile Leu Leu Leu Pro Leu Leu Ile Val  
 1 5 10 15  
 Phe Cys Ile Glu Ser Phe Ile Lys Arg Leu Ile Pro Lys Lys Lys Lys  
 20 25 30  
 Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45  
 Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Asn Thr Lys Leu Val  
 50 55 60  
 Leu Trp Asp Ile Asn Lys Asn Gly Ile Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80  
 Arg Lys Leu Gly Ala Gln Val His Pro Phe Val Val Asp Cys Ser Gln

```

      85      90      95
Arg Glu Glu Ile Tyr Ser Ala Val Arg Lys Val Lys Glu Glu Val Gly
      100      105      110
Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ala Asp
      115      120      125
Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
      130      135      140
Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Met
      145      150      155      160
Lys Asn Asn His Gly His Val Val Thr Val Ala Ser Ala Ala Gly His
      165      170      175
Thr Val Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
      180      185      190
Val Gly Phe His Arg Ala Leu Thr Asp Glu Leu Ala Ala Leu Gly Cys
      195      200      205
Thr Gly Val Arg Thr Ser Cys Leu Cys Pro Asn Phe Ile Asn Thr Gly
      210      215      220
Phe Ile Lys Asn Pro Ser Thr Asn Leu Gly Pro Thr Leu Glu Pro Glu
      225      230      235      240
Glu Val Val Glu His Leu Met His Gly Ile Leu Thr Asn Gln Lys Met
      245      250      255
Ile Phe Val Pro Gly Ser Ile Ala Leu Leu Thr Val Leu Glu Arg Val
      260      265      270
Phe Pro Glu Arg Phe Leu Asp Val Leu Lys His Arg Ile Asn Val Lys
      275      280      285
Phe Asp Ala Val Val Gly Tyr Lys Asp Lys
      290      295

```

&lt;210&gt; 647

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 647

```

Met Asn Ser Val Pro Thr Gln Leu Ile Leu Val Leu Thr Ser Leu Leu
  1      5      10      15
Leu Ile Leu Pro Gly Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
      20      25      30
Leu Leu Leu Gly Val Val Leu Ser Val Thr Gly Ile Cys Ala Cys Leu
      35      40      45
Gly Ile Tyr Ala Arg Lys Arg Asn Gly Gln Ile
      50      55

```

&lt;210&gt; 648

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 648

```

Val Leu Ser Thr Ala Pro Pro Thr Met Arg Pro Ala Pro Gln Pro Gln
  1      5      10      15
Asp Cys Pro Ala Ser Ile Cys Leu Asn Gly Gly Ser Cys Arg Val Gly
      20      25      30
Ala Lys His His Leu Glu Cys Leu Cys Pro Glu Gly Phe Ile Gly Leu
      35      40      45
Tyr Cys Glu Ser Pro Val Glu Gln Arg Thr Lys Pro Ser Ser Ile Pro
      50      55      60

```

```

Asp Thr Pro Arg Pro Pro Arg Leu Leu Pro Leu Arg Ile Glu Pro Val
65          70          75          80
Ser Pro Thr Ser Leu Arg Val Glu Leu Gln Arg Tyr Leu Gln Gly Asn
85          90          95
Thr Val Gln Leu Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu Ser Gly
100        105        110
Pro Asp Lys Arg Leu Val Thr Leu Arg Leu Pro Ala Ser Leu Ala Glu
115        120        125
Tyr Thr Val Thr Gln Leu Arg Pro Asn Ala Thr Tyr Ser Ile Cys Val
130        135        140
Thr Ala Leu Gly Ala Gly Arg Thr Pro Glu Gly Glu Glu Ala Cys Gly
145        150        155        160
Glu Ala Asn Thr Pro Gln Ala Val Arg Ser Asn His Ala Pro Val Thr
165        170        175
Gln Ala Arg Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala
180        185        190
Ala Val Leu Leu Ala Val Leu Ala Ala Ser Gly Ala Val Tyr Cys Val
195        200        205
Arg Arg Ala Arg Ala Ser Ser Thr Ala Gln Asp Lys Gly Gln Val Gly
210        215        220
Pro Gly Thr Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro Leu Glu
225        230        235        240
Pro Gly Ser Lys Ala Ser Glu Gly Gly Gly Glu Ala Leu Ser Gly Gly
245        250        255
Pro Glu Cys Glu Val Pro Leu Met Gly Tyr Pro Gly Pro Ser Leu Gln
260        265        270
Gly Val Leu Pro Ala Gln Pro Tyr Ile
275          280

```

<210> 649  
 <211> 88  
 <212> PRT  
 <213> Rat

```

<400> 649
Leu Gly Ser Val Ser Val Thr Thr Ile Glu Pro Cys Val Gln Val Gly
1          5          10          15
Ser Pro Ala Arg His Ser Leu His Pro Pro Leu Cys Ile Ser Ile Gly
20        25        30
Ala Thr Val Pro Tyr Phe Ala Glu Gly Ser Gly Gly Pro Val Pro Thr
35        40        45
Thr Ser Ala Leu Ile Leu Pro Glu Tyr Ser Ser Trp Gly Tyr Pro
50        55        60
Tyr Glu Ala Pro Pro Ser Tyr Glu Gln Ser Cys Gly Ala Gly Gly Thr
65        70        75        80
Asp Val Gly Leu Ile Pro Gly Ser
85

```

<210> 650  
 <211> 290  
 <212> PRT  
 <213> Rat

```

<400> 650
Glu Val Asp Pro Asp Leu Lys Cys Ala Leu Cys His Lys Val Leu Glu
1          5          10          15
Asp Pro Leu Thr Thr Pro Cys Gly His Val Phe Cys Ala Gly Cys Val

```

```

                20                25                30
Leu Pro Trp Val Val Gln Glu Gly Ser Cys Pro Ser Arg Cys Arg Gly
   35   40   45
Arg Leu Ser Ala Lys Glu Leu Asn His Val Leu Pro Leu Lys Arg Leu
   50   55   60
Ile Leu Lys Leu Asp Ile Lys Cys Ala His Ala Arg Gly Cys Gly
   65   70   75   80
Arg Val Val Lys Leu Gln Asp Leu Pro Glu His Leu Glu Arg Cys Asp
   85   90   95
Phe Ala Pro Ala Arg Cys Arg His Ala Gly Cys Gly Gln Leu Leu Leu
  100  105  110
Arg Arg Asp Val Glu Ala His Met Arg Asp Ala Cys Asp Ala Arg Pro
  115  120  125
Val Gly Arg Cys Gln Glu Gly Cys Gly Leu Pro Leu Thr His Gly Glu
  130  135  140
Gln Arg Ala Gly Gly His Cys Cys Ala Arg Ala Leu Arg Ala His Asn
  145  150  155  160
Gly Ala Leu Gln Ala Arg Leu Gly Ala Leu His Lys Ala Leu Lys Lys
  165  170  175
Glu Ala Leu Arg Ala Gly Lys Arg Glu Lys Ser Leu Val Ala Gln Leu
  180  185  190
Ala Ala Ala Gln Leu Glu Leu Gln Met Thr Ala Leu Arg Tyr Gln Lys
  195  200  205
Lys Phe Thr Glu Tyr Ser Ala Arg Leu Asp Ser Leu Ser Arg Cys Val
  210  215  220
Ala Ala Pro Pro Gly Gly Lys Gly Glu Glu Thr Lys Ser Val Thr Leu
  225  230  235  240
Val Leu His Arg Asp Ser Gly Ser Leu Gly Phe Asn Ile Ile Gly Gly
  245  250  255
Arg Pro Cys Val Asp Asn Gln Asp Gly Ser Ser Ser Glu Gly Ile Phe
  260  265  270
Val Ser Lys Ile Val Asp Ser Gly Pro Ala Ala Lys Lys Arg Pro Ala
  275  280  285
Asn Ser
  290

```

<210> 651  
 <211> 202  
 <212> PRT  
 <213> Rat

```

<400> 651
Met Ala Arg Pro Arg Pro Arg Glu Tyr Lys Ala Gly Asp Leu Val Phe
  1     5     10     15
Ala Lys Met Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Glu Leu
  20     25     30
Pro Glu Gly Ala Val Lys Pro Pro Ala Asn Lys Tyr Pro Ile Phe Phe
  35     40     45
Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
  50     55     60
Tyr Lys Glu Tyr Lys Asp Lys Phe Gly Lys Ser Asn Lys Arg Lys Gly
  65     70     75     80
Phe Asn Glu Gly Leu Trp Glu Ile Glu Asn Asn Pro Gly Val Lys Phe
  85     90     95
Thr Gly Tyr Gln Thr Ile Gln Gln Gln Ser Ser Ser Glu Thr Glu Gly
  100    105    110
Glu Gly Gly Asn Thr Ala Asp Ala Ser Ser Glu Glu Glu Gly Asp Arg

```

```

      115      120      125
Val Glu Asp Gly Lys Gly Lys Arg Lys Asn Glu Lys Gly Gly Ser Lys
  130      135      140
Arg Lys Lys Ser Tyr Thr Ser Lys Lys Ser Ser Lys Gln Ser Arg Lys
  145      150      155
Ser Pro Gly Asp Glu Asp Asp Lys Asp Cys Lys Glu Glu Glu Asn Lys
      165      170      175
Ser Ser Ser Glu Gly Gly Asp Ala Gly Asn Asp Thr Arg Asn Thr Thr
  180      185      190
Ser Asp Leu Gln Lys Ala Gly Glu Gly Thr
      195      200

```

<210> 652  
 <211> 79  
 <212> PRT  
 <213> Rat

```

<400> 652
Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe
  1      5      10      15
Asp Arg Val Lys Met Gly Phe Val Met Gly Cys Ala Val Gly Met Ala
      20      25      30
Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu Arg Ile Gly Met Arg
      35      40      45
Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr Met Met Gln Ser Gly
  50      55      60
Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met Gly Ile Arg Cys
  65      70      75

```

<210> 653  
 <211> 555  
 <212> PRT  
 <213> Rat

```

<400> 653
Met Pro Val Asn Leu Gly Gln Ala Leu Gly Leu Leu Pro Phe Leu Ala
  1      5      10      15
Lys Ala Glu Asp Ala Thr Phe Ser Gly Ser Asp Val Ile Gln Gln Arg
      20      25      30
Glu Leu Ala Asn Pro Glu Thr Ala Arg Gln Leu Phe Arg Gln Phe Arg
      35      40      45
Tyr Gln Val Met Ser Gly Pro Gln Glu Thr Leu Arg Gln Leu Arg Lys
  50      55      60
Leu Cys Phe Gln Trp Leu Arg Pro Glu Val His Thr Lys Glu Gln Ile
  65      70      75
Leu Glu Ile Leu Met Leu Glu Gln Phe Leu Thr Ile Leu Pro Gly Glu
      85      90      95
Ile Gln Met Trp Val Arg Lys Gln Cys Pro Gly Ser Gly Glu Glu Ala
      100      105      110
Val Thr Leu Val Glu Ser Leu Lys Gly Asp Pro Gln Lys Leu Trp Gln
      115      120      125
Trp Ile Ser Ile Gln Val Leu Gly Gln Glu Ile Pro Phe Glu Lys Glu
      130      135      140
Asn Ser Ala Arg Cys Arg Gly Asp Lys Val Glu Pro Ala Leu Glu Ala
  145      150      155
Glu Pro Thr Val Glu Val Val Pro Gln Asp Leu Pro Leu Gln Asn Thr
      165      170      175

```

```

Ser Ser Ala Pro Gly Glu Leu Leu Ser His Gly Val Lys Glu Glu Ser
180 185 190
Asp Met Glu Pro Glu Leu Ala Leu Ala Ala Ser Gln Leu Pro Ala Arg
195 200 205
Ser Glu Glu Arg Pro Thr Arg Asp Gln Glu Val Gly Thr Ala Leu Leu
210 215 220
Pro Ser Leu Gln Glu Glu Gln Trp Arg His Leu Asp Ser Thr Gln Lys
225 230 235 240
Glu Gln Tyr Trp Asp Leu Met Leu Glu Thr Tyr Gly Lys Met Val Ser
245 250 255
Gly Ala Gly Ile Ser Asn Ser Lys Pro Asp Leu Thr Asn Met Ala Glu
260 265 270
Tyr Gly Glu Glu Leu Val Gly Leu His Leu His Ser Ala Glu Lys Met
275 280 285
Ala Arg Ala Pro Cys Lys Glu Asp Arg Gln Glu Asn Asp Lys Glu Asn
290 295 300
Leu Asn Leu Glu Asn His Arg Asp Gln Gly Cys Leu Asp Val Phe Asp
305 310 315 320
Gln Ala Pro Gly Glu Ala Pro Pro Gln Thr Ala Leu Ser Asp Phe Phe
325 330 335
Gly Glu Ser Glu Pro His His Phe Gly Gly Glu Ser Val Pro Glu Ala
340 345 350
Leu Glu Asn Leu Gln Gly Glu Gly Thr Gly Ala His Leu Phe Pro His
355 360 365
Glu Arg Gly Ser Gly Lys Gln Leu Gly Gln His Ile Gln Ser Ser Ser
370 375 380
Ser Gly Glu Leu Ser Ala Leu Trp Leu Glu Glu Lys Arg Glu Ala Ser
385 390 395 400
Gln Lys Gly Gln Ala Arg Ala Pro Met Ala Gln Lys Leu Pro Thr Cys
405 410 415
Arg Glu Cys Gly Lys Thr Phe Tyr Arg Asn Ser Gln Leu Val Phe His
420 425 430
Gln Arg Thr His Thr Gly Glu Thr Tyr Phe His Cys Arg Ile Cys Lys
435 440 445
Lys Ala Phe Leu Arg Ser Ser Asp Phe Val Lys His Gln Arg Thr His
450 455 460
Thr Gly Glu Lys Pro Cys Lys Cys Asp Tyr Cys Gly Lys Gly Phe Ser
465 470 475 480
Asp Phe Ser Gly Leu Arg His His Glu Lys Ile His Thr Gly Glu Lys
485 490 495
Pro Tyr Lys Cys Pro Ile Cys Glu Lys Ser Phe Ile Gln Arg Ser Asn
500 505 510
Phe Asn Arg His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys
515 520 525
Thr His Cys Gly Lys Arg Phe Ser Trp Ser Ser Ser Leu Asp Lys His
530 535 540
Gln Arg Ser His Leu Gly Lys Lys Pro Cys Pro
545 550 555

```

&lt;210&gt; 654

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 654

```

Leu Ala Tyr Tyr Asn Pro Phe Tyr Phe Leu Ser Ala Ala Ala Pro Gly
1 5 10 15

```



```

Pro Gly Ala Ala Thr Ser Ala Gly Ala Thr Pro Thr Ala Val Ala Gly
      20      25      30
Leu Thr Ala Arg Ala Pro His Val Gln Ala Ser Ala Arg Ala Val Pro
      35      40      45
Val Thr Arg Val Gly Ser Ala Ala Pro Ala Arg Thr Ala Ser Asp Thr
      50      55      60
Gly Arg Gln Ala Gly Arg Glu Tyr Val Ile Pro Ser Leu Ala His Arg
      65      70      75      80
Phe Met Ala Glu Met Val Asp Phe Phe Ile Leu Phe Phe Ile Lys Ala
      85      90      95
Thr Ile Val Leu Ser Ile Met His Leu Ser Gly Ile Lys Asp Ile Ser
      100      105      110
Lys Phe Ala Met His Tyr Ile Ile Glu Glu Ile Asp Glu Asp Thr Ser
      115      120      125
Met Glu Asp Leu Gln Lys Met Met Ile Val Ala Leu Ile Tyr Arg Leu
      130      135      140
Leu Val Cys Phe Tyr Glu Ile Ile Cys Ile Trp Gly Ala Gly Gly Ala
      145      150      155      160
Thr Pro Gly Lys Phe Leu Leu Gly Leu Arg Val Val Thr Cys Asp Thr
      165      170      175
Ser Val Leu Ile Ala Pro Ser Arg Val Leu Val Ile Pro Ser Ser Asn
      180      185      190
Val Ser Ile Thr Thr Ser Thr Ile Arg Ala Leu Ile Lys Asn Phe Ser
      195      200      205
Ile Ala Ser Phe Phe Pro Ala Phe Ile Thr Leu Leu Phe Phe Gln His
      210      215      220
Asn Arg Thr Ala Tyr Asp Ile Val Ala Gly Thr Ile Val Val Lys Arg
      225      230      235      240
Asn Gly Val Arg

```

<210> 655  
 <211> 265  
 <212> PRT  
 <213> Rat

```

<400> 655
Met Gly Leu Leu Phe Leu Val Leu Leu Ser Pro Leu Ser Cys Val Leu
  1      5      10      15
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Gly Leu His Gly
      20      25      30
Arg Thr Leu Gly Asn Gly Tyr Gly Glu Gly Leu Phe Asn Gly Val Lys
      35      40      45
Leu Val Val Glu Thr Thr Glu Ser Leu Phe Ser His Gln Gly Ala
      50      55      60
Ser Val Thr Leu Pro Cys His Tyr His Tyr Glu Pro Ala Leu Ala Ser
      65      70      75      80
Pro Arg His Val Arg Ile Lys Trp Trp Lys Leu Ser Glu Asn Gly Thr
      85      90      95
Pro Glu Gln Asp Val Leu Val Ala Ile Gly Gln Arg His Arg Ser Phe
      100      105      110
Gly Asp Tyr Gln Gly Arg Val Gln Leu Arg Gln Asp Lys Glu Gln Glu
      115      120      125
Val Ser Leu Glu Leu Arg Asp Leu Arg Leu Glu Asp Ser Gly Arg Tyr
      130      135      140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
      145      150      155      160

```

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Pro Arg Glu Gly Arg  
 165 170 175  
 Tyr Gln Leu Asn Phe His Glu Ala Gln Gln Val Cys Gln Glu Gln Asp  
 180 185 190  
 Ala Val Val Ala Thr Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly  
 195 200 205  
 Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Ser Ser Cys Arg  
 210 215 220  
 Phe Gly Thr Ser Ser Cys Arg Ile Arg His Glu Ala Cys Arg Arg Pro  
 225 230 235 240  
 Leu Trp Cys Gly Asp Pro Arg Val Asn Pro Pro Thr Pro Cys Leu Thr  
 245 250 255  
 Arg Arg Gln Asn Leu Gln Leu Arg Thr  
 260 265

&lt;210&gt; 656

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 656

Met Ala Val Cys Pro Tyr Gly Ala Ala Ala Val Val Met Ala Leu Leu  
 1 5 10 15  
 Ser Ala Ala Ile Ala Phe His Trp Ser Pro Leu Leu Ala Val Leu Gln  
 20 25 30  
 Arg Ala Leu Ser Leu His Thr Ala His Ala Thr Lys Asp Met Asp Asn  
 35 40 45  
 Leu Phe Gln Leu Val Arg Asn Ile Val Pro Ala Leu Thr Ser Lys Lys  
 50 55 60  
 His Lys Gly Gln Asp Gly Arg Ile Gly Ile Val Gly Gly Cys Gln Glu  
 65 70 75 80  
 Tyr Thr Gly Ala Pro Tyr Phe Ala Gly Ile Ser Ala Leu Lys Val Gly  
 85 90 95  
 Ala Asp Leu Thr His Val Phe Cys Ala Arg Glu Ala Ala Pro Val Ile  
 100 105 110  
 Lys Ser Tyr Ser Pro Glu Leu Ile Val His Pro Val Leu Asp Ser Ser  
 115 120 125  
 Asp Ala Val Glu Glu Val Lys Lys Trp Leu Pro Arg Leu His Ala Leu  
 130 135 140  
 Val Val Gly Pro Gly Leu Gly Arg Asp Asp Leu Leu Leu Asn Asn Val  
 145 150 155 160  
 Arg Gly Ile Leu Glu Ser Thr Lys Ala Arg Asp Ile Pro Val Val Ile  
 165 170 175  
 Asp Ala Asp Gly Leu Trp Leu Ile Ala Gln Arg Pro Ala Leu Val His  
 180 185 190  
 Gly Tyr Gln Lys Ala Val Leu Thr Pro Asn His Val Glu Phe Ser Arg  
 195 200 205  
 Leu Trp Asp Ala Val Leu Ser Ser Pro Met Asp Thr Ser Asn His Ser  
 210 215 220  
 Gly Ser Val Leu Lys Leu Ser Gln Ala Leu Gly Asn Ile Thr Ile Val  
 225 230 235 240  
 Gln Lys Gly Glu Gln Asp Leu Ile Ser Asn Gly Gln Gln Val Leu Val  
 245 250 255  
 Cys Asn Gln Glu Gly Ser Ser Arg Arg Cys Gly Gly Gln Gly Asp Leu  
 260 265 270  
 Leu Ser Gly Ser Leu Gly Val Met Ala His Trp Ala Leu Arg Ala Gly  
 275 280 285

Pro Glu Lys Thr Asn Gly Ser Ser Pro Leu Leu Val Ala Ala Trp Gly  
 290 295 300  
 Ala Cys Thr Leu Thr Arg Glu Cys Asn His Leu Ala Phe Gln Lys Tyr  
 305 310 315 320  
 Gly Arg Ser Thr Thr Thr Thr Asp Met Ile Ala Glu Val Gly Ala Ala  
 325 330 335  
 Phe Ser Lys Leu Phe Thr Thr  
 340

<210> 657  
 <211> 61  
 <212> PRT  
 <213> Rat

<400> 657  
 Met Pro Cys Trp Ser Leu Tyr Gln Leu Met Val Leu Tyr Gln Ile Ile  
 1 5 10 15  
 Ile Leu Phe Phe Leu Phe Lys Gln Val Ser Val Arg Thr Cys Tyr Leu  
 20 25 30  
 Ser Thr Glu Gly Lys Pro Cys Gly Ser Val Leu Phe Ala Cys Lys Ser  
 35 40 45  
 Leu Gln Gln Cys Leu Leu Thr Val Leu Val Thr Pro Val  
 50 55 60

<210> 658  
 <211> 1172  
 <212> PRT  
 <213> Rat

<400> 658  
 Met Leu Trp Ala Leu Ala Leu Leu Ala Leu Gly Ile Gly Pro Arg Ala  
 1 5 10 15  
 Tyr Ala Gly Asp His Gly Glu Asp Thr Ala Phe Asp Leu Phe Ser Ile  
 20 25 30  
 Ser Asn Ile Asn Arg Lys Thr Ile Gly Ala Lys Gln Phe Arg Gly Pro  
 35 40 45  
 Asp Pro Gly Val Pro Ala Tyr Arg Phe Val Arg Phe Asp Tyr Val Pro  
 50 55 60  
 Pro Val Asn Thr Asp Asp Leu Asn Arg Ile Val Lys Leu Ala Arg Arg  
 65 70 75 80  
 Lys Glu Gly Phe Phe Leu Thr Ala Gln Leu Lys Gln Asp Arg Lys Ser  
 85 90 95  
 Arg Gly Thr Leu Leu Val Leu Glu Gly Pro Gly Thr Ser Gln Arg Gln  
 100 105 110  
 Phe Glu Ile Val Ser Asn Gly Pro Gly Asp Thr Leu Asp Leu Asn Tyr  
 115 120 125  
 Trp Val Glu Gly His Gln His Thr Asn Phe Leu Glu Asp Val Gly Leu  
 130 135 140  
 Ala Asp Ser Gln Trp Lys Asn Val Thr Val Gln Val Ala Ser Asp Thr  
 145 150 155 160  
 Tyr Ser Leu Tyr Val Gly Cys Asp Leu Ile Asp Ser Val Thr Leu Glu  
 165 170 175  
 Glu Pro Phe Tyr Glu Gln Leu Glu Ala Asp Lys Ser Arg Met Tyr Val  
 180 185 190  
 Ala Lys Gly Ala Ser Arg Glu Ser His Phe Arg Gly Leu Leu Gln Asn  
 195 200 205  
 Val His Leu Val Phe Ala Asp Ser Val Glu Asp Ile Leu Ser Lys Lys

210						215					220				
Gly	Cys	Gln	His	Ser	Gln	Gly	Ala	Glu	Val	Asn	Thr	Ile	Ser	Glu	His
225					230					235					240
Thr	Glu	Thr	Leu	His	Leu	Ser	Pro	His	Ile	Thr	Thr	Asp	Leu	Val	Val
				245						250					255
Gln	Gly	Val	Glu	Lys	Ala	Gln	Glu	Val	Cys	Thr	His	Ser	Cys	Glu	Glu
			260					265					270		
Leu	Ser	Asn	Met	Met	Asn	Glu	Leu	Ser	Gly	Leu	His	Val	Met	Val	Asn
		275				280						285			
Gln	Leu	Ser	Lys	Asn	Leu	Glu	Arg	Val	Ser	Ser	Asp	Asn	Gln	Phe	Leu
290						295					300				
Leu	Glu	Leu	Ile	Gly	Gly	Pro	Leu	Lys	Thr	Arg	Asn	Met	Ser	Ala	Cys
305					310					315					320
Val	Gln	Glu	Gly	Arg	Ile	Phe	Ala	Glu	Asn	Glu	Thr	Trp	Val	Val	Asp
			325						330						335
Ser	Cys	Thr	Thr	Cys	Thr	Cys	Lys	Lys	Phe	Lys	Thr	Val	Cys	Asn	Gln
			340					345					350		
Ile	Thr	Cys	Ser	Pro	Ala	Thr	Cys	Ala	Asn	Pro	Ser	Leu	Val	Glu	Gly
		355					360						365		
Glu	Cys	Cys	Pro	Ser	Cys	Ser	His	Ser	Ala	Asp	Asn	Asp	Glu	Gly	Trp
370						375					380				
Ser	Pro	Trp	Ala	Glu	Trp	Thr	Glu	Cys	Ser	Val	Thr	Cys	Gly	Ser	Gly
385					390					395					400
Thr	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp	Val	Thr	Ser	Asn	Thr	Cys	Leu
			405						410					415	
Gly	Pro	Ser	Ile	Gln	Thr	Arg	Thr	Cys	Ser	Leu	Gly	Lys	Cys	Asp	Thr
			420					425						430	
Arg	Ile	Arg	Gln	Asn	Gly	Gly	Trp	Ser	His	Trp	Ser	Pro	Trp	Ser	Ser
		435					440					445			
Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn	Val	Thr	Arg	Ile	Arg	Leu	Cys
450						455					460				
Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly	Lys	Asn	Cys	Lys	Gly	Ser	Gly
465					470					475					480
Arg	Glu	Thr	Lys	Ala	Cys	Gln	Arg	Ala	Pro	Cys	Pro	Ile	Asp	Gly	Arg
			485						490					495	
Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	Cys	Thr	Val	Thr	Cys	Ala	Gly
		500						505					510		
Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys	Asn	Ser	Pro	Glu	Pro	Gln	Tyr
		515					520					525			
Gly	Gly	Lys	Asp	Cys	Val	Gly	Asp	Val	Thr	Glu	His	Gln	Met	Cys	Asn
530						535					540				
Lys	Arg	Ser	Cys	Pro	Ile	Asp	Gly	Cys	Leu	Ser	Asn	Pro	Cys	Phe	Pro
545					550					555					560
Gly	Ala	Lys	Cys	Asn	Ser	Phe	Pro	Asp	Gly	Ser	Trp	Ser	Cys	Gly	Ser
				565					570					575	
Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	Thr	His	Cys	Glu	Asp	Leu	Asp
		580						585				590			
Glu	Cys	Ala	Val	Val	Ala	Asp	Ile	Cys	Phe	Ser	Ile	Asn	Lys	Ala	Ser
		595					600					605			
Arg	Cys	Val	Asn	Thr	Asn	Pro	Gly	Phe	His	Cys	Leu	Pro	Cys	Pro	Pro
610						615					620				
Arg	Tyr	Lys	Gly	Thr	Gln	Pro	Phe	Gly	Ile	Gly	Leu	Glu	Asp	Ala	Lys
625					630					635					640
Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	Asn	Pro	Cys	Lys	Asp	Lys	Thr
			645						650					655	
His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	Ile	Tyr	Leu	Gly	His	Phe	Ser
			660					665					670		

```

Asp Pro Met Tyr Lys Cys Glu Cys Gln Thr Gly Tyr Ala Gly Asp Gly
675 680 685
Leu Ile Cys Gly Glu Asp Ser Asp Leu Asp Gly Trp Pro Asn Ser Asn
690 695 700
Leu Val Cys Ala Thr Asn Ala Thr Tyr His Cys Val Lys Asp Asn Cys
705 710 715 720
Pro Lys Leu Pro Asn Ser Gly Gln Glu Asp Phe Asp Lys Asp Gly Ile
725 730 735
Gly Asp Ala Cys Asp Glu Asp Asp Asp Asn Asp Gly Val Ser Asp Glu
740 745 750
Lys Asp Asn Cys Pro Leu Leu Phe Asn Pro Arg Gln Leu Asp Tyr Asp
755 760 765
Lys Asp Glu Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Val His Asn
770 775 780
Gln Ala Gln Ile Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ser
785 790 795 800
Val Asp Ile Asp Gly Asp Asp Val Phe Asn Glu Arg Asp Asn Cys Pro
805 810 815
Tyr Val Tyr Asn Thr Asp Gln Arg Asp Thr Asp Gly Asp Gly Val Gly
820 825 830
Asp His Cys Asp Asn Cys Pro Leu Met His Asn Pro Asp Gln Met Asp
835 840 845
Gln Asp Asn Asp Leu Val Gly Asp Gln Cys Asp Asn Asn Glu Asp Ile
850 855 860
Asp Asp Asp Gly His Gln Asn Asn Gln Asp Asn Cys Pro Tyr Ile Ser
865 870 875 880
Asn Ser Asn Gln Ala Asp His Asp Asn Asp Gly Lys Gly Asp Ala Cys
885 890 895
Asp Ser Asp Asp Asp Asn Asp Gly Val Pro Asp Asp Arg Asp Asn Cys
900 905 910
Arg Leu Val Phe Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg
915 920 925
Gly Asp Ile Cys Lys Asp Asp Phe Asp Asn Asp Asn Val Pro Asp Ile
930 935 940
Asp Asp Val Cys Pro Glu Asn Asn Ala Ile Thr Glu Thr Asp Phe Arg
945 950 955 960
Asn Phe Gln Met Val Pro Leu Asp Pro Lys Gly Thr Thr Gln Ile Asp
965 970 975
Pro Asn Trp Val Ile Arg His Gln Gly Lys Glu Leu Val Gln Thr Ala
980 985 990
Asn Ser Asp Pro Gly Ile Ala Val Gly Phe Asp Glu Phe Gly Ser Val
995 1000 1005
Asp Phe Ser Gly Thr Phe Tyr Val Asn Thr Asp Arg Asp Asp Asp Tyr
1010 1015 1020
Ala Gly Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val
1025 1030 1035 1040
Met Trp Lys Gln Val Thr Gln Thr Tyr Trp Glu Asp Lys Pro Ser Arg
1045 1050 1055
Ala Tyr Gly Tyr Ser Gly Val Ser Leu Lys Val Val Asn Ser Thr Thr
1060 1065 1070
Gly Thr Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr
1075 1080 1085
Glu Gly Gln Val Arg Thr Leu Trp His Asp Pro Lys Asn Ile Gly Trp
1090 1095 1100
Lys Asp Tyr Thr Ala Tyr Arg Trp His Leu Ile His Arg Pro Lys Thr
1105 1110 1115 1120
Gly Tyr Met Arg Val Leu Val His Glu Gly Lys Gln Val Met Ala Asp

```

```

          1125          1130          1135
Ser Gly Pro Ile Tyr Asp Gln Thr Tyr Ala Gly Gly Arg Leu Gly Leu
          1140          1145          1150
Phe Val Phe Ser Gln Glu Met Val Tyr Phe Ser Asp Leu Lys Tyr Glu
          1155          1160          1165
Cys Arg Asp Ala
          1170

```

&lt;210&gt; 659

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 659

```

Met Glu Leu Leu Ser Arg Val Leu Leu Trp Lys Leu Val Leu Leu Gln
 1          5          10          15
Ser Ser Ala Val Leu Ser Ser Gly Ser Pro Gly Thr Ala Ala Ser
          20          25          30
Ser Ser Val Val Ser Glu Ser Ala Val Ser Trp Ala Ala Gly Thr Gln
          35          40          45
Ala Val Leu Arg Cys Gln Ser Pro Arg Met Val Trp Thr Gln Asp Arg
 50          55          60
Leu His Asp Arg Gln Arg Val Val His Trp Asp Leu Ser Gly Gly Pro
 65          70          75          80
Gly Ser Gln Gly Arg Arg Leu Val Asp Met Tyr Ser Ala Gly Glu Gln
          85          90          95
Arg Val Tyr Gln Pro Arg Asp Arg Asp Arg Leu Leu Leu Ser Pro Ser
          100          105          110
Ala Phe His Asp Gly Asn Phe Ser Leu Leu Ile Arg Ala Val Glu Arg
          115          120          125
Gly Asp Glu Gly Val Tyr Thr Cys Asn Leu His His His Tyr Cys His
          130          135          140
Leu Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Asp Pro Leu
 145          150          155          160
Leu Ser Arg Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Val Val Ala
          165          170          175
Leu Gly Ala Pro Ala Leu Met Thr Cys Val Asn Arg Glu His Leu Trp
          180          185          190
Thr Asp Arg His Leu Glu Glu Ala Gln Gln Val Val His Trp Asp Arg
          195          200          205
Gln Leu Pro Gly Val Pro His Asp Arg Ala Asp Arg Leu Leu Asp Leu
 210          215          220
Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro Pro Phe Leu Arg Asp
 225          230          235          240
Arg Val Ser Val Asn Thr Asn Ala Phe Ala Arg Gly Asp Phe Ser Leu
          245          250          255
Arg Ile Asp Asp Leu Glu Pro Ala Asp Glu Gly Ile Tyr Ser Cys His
          260          265          270
Leu His His His Tyr Cys Gly Leu His Glu Arg Arg Val Phe His Leu
          275          280          285
Arg Val Thr Glu Pro Val Phe Glu Pro Pro Ala Arg Ala Ser Pro Gly
 290          295          300
Asn Gly Ser Gly His Asn Ser Val Pro Ser Pro Asp Pro Thr Met Ala
 305          310          315          320
Arg Gly His Ser Ile Ile Asn Val Ile Val Pro Glu Asp His Thr His
          325          330          335
Phe Phe Gln Gln Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile

```

```

          340          345          350
Leu Leu Leu Ile Thr Val Val Leu Ala Thr Arg His Arg His Ser Gly
          355          360          365
Gly Cys Lys Thr Ser Asp Arg Lys Ala Gly Lys Ser Lys Gly Lys Asp
          370          375          380
Val Asn Met Met Glu Phe Ala Ile Ala Thr Arg Asp Gln Ala Pro Tyr
385          390          395          400
Arg Thr Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
          405          410          415
Arg Ala Gly Leu Ala His Ser Pro Leu Pro Ala Lys Asp Val Asp Leu
          420          425          430
Asp Lys Glu Phe Arg Lys Glu Tyr Cys Lys
          435          440

```

<210> 660  
 <211> 218  
 <212> PRT  
 <213> Rat

```

<400> 660
Gln Leu Ser Pro Leu Asp Phe Pro His Leu Pro His Gln Ser Glu Leu
 1          5          10          15
Ser Ser Thr Ala Arg Ala Arg Pro Pro Asn Ala Ala Ile Asp Arg Arg
          20          25          30
Gln Gly Gln Leu Leu Phe Ser Cys Pro Trp Ser Cys Ile Thr Ser Thr
          35          40          45
His Thr Phe Ile Ala Ser Ser Thr Val Leu Pro Gly Lys Val Gln Ala
          50          55          60
Pro Phe Ser Arg Val Leu Gln Leu Val Arg Gly Arg Ala Ser Ser Pro
65          70          75          80
Lys Leu Met Thr Leu Trp Gly Ala Phe Pro Pro Ala Arg Gly Asp Glu
          85          90          95
Val Leu Gly Arg Gly Trp Asn Ile Thr Ser Val Pro Leu Pro Ser His
          100          105          110
Ser Arg Gln Val Ala Gly Ser Ala Ser His Thr His Thr Leu Gly Ala
          115          120          125
Ala Ser Pro Thr Pro Leu Ser Pro Gly Pro Ala Pro Leu Cys Ser Thr
          130          135          140
Met Leu Pro Gly Gln Gly Thr Gly Pro Thr Leu Pro Ser Ala Gly Thr
145          150          155          160
Val Pro Ala Leu Pro Ser Ala Ala Thr Gly Glu Gly Trp Gly Gln Val
          165          170          175
Ser Arg Gly Pro His Pro Val Arg Asp Gly Val Val His Ile Pro Trp
          180          185          190
Thr Cys Thr Trp Cys Leu Met Ala Ala Pro Thr Arg Asn Thr Pro Met
          195          200          205
Ser Ser Ile Gly Asn Met Ser His Gly His
          210          215

```

<210> 661  
 <211> 108  
 <212> PRT  
 <213> Rat

```

<400> 661
Met Ser Leu Ile Gln Ala Ile Val Tyr Lys Val His Ser Phe Ser Cys
 1          5          10          15

```

```

Asp Leu Glu Tyr Ile Tyr Asn Leu Asp Gly Ile Gln Val Arg Asn Lys
      20      25      30
Ala Ile Gly Cys Pro Gln Arg His Gln Leu Pro Ala Leu Gln Glu Ala
      35      40      45
Thr Ala Phe Ala Gly Val His Arg Pro Leu Gln Ile His Pro Leu Gly
      50      55      60
Arg Gly Leu Arg Pro Trp Glu Gln Gln Gln Arg His Cys Gly His
      65      70      75      80
Ile Trp Pro Gly Trp Glu Pro Leu Arg Ser Asp Ser Leu Ala Leu Gly
      85      90      95
Thr Ala Ser Cys Glu Thr Asn Arg Asn Ser Pro Leu
      100      105

```

<210> 662  
 <211> 516  
 <212> PRT  
 <213> Rat

```

<400> 662
Asn Gln Gly Arg Arg Gly Arg Ser Ser Lys Pro Ser Ile Lys Thr Pro
  1      5      10      15
Glu Pro Ile Val Pro Thr Gly Pro Glu Leu Gln Pro Leu Thr Ser Ala
      20      25      30
Glu Gln Pro Val Thr Pro Asn Leu Thr Ser Arg Ala Ser Arg Gly Arg
      35      40      45
Ser Asn Lys Ser Ile Arg Thr Pro Glu Pro Val Val Gln Thr Gly Pro
      50      55      60
Glu Phe His Pro Ser Thr Ser Ser Glu Gln Ser Asp Thr Pro Glu Pro
      65      70      75      80
Ser Ser Gln Gly Arg Thr Arg Arg Ser Val Arg Thr Pro Glu Ala Ser
      85      90      95
Val Ser Thr Thr Pro Ala Leu Gln Pro Ser Thr Ser Lys Lys Gln Pro
      100      105      110
Thr Pro Lys Pro Thr Ala Leu Val Thr Arg Gly Arg Thr His Lys Pro
      115      120      125
Ser Thr Glu Gly Leu Glu Ser Val Gly Pro Val Ala Pro Asp Phe Glu
      130      135      140
Pro Pro Thr Ser Thr Asp His Leu Ala Thr Ser Lys Val Thr Gly Gln
      145      150      155      160
Ser Leu Thr Leu Gln Ser Ser Pro Val Ser Ala Ser Pro Val Ser Thr
      165      170      175
Thr Pro Glu Leu Lys Pro Pro Val Pro Ile Ala Gln Pro Leu Thr Leu
      180      185      190
Glu Pro Val Pro Gln Thr Ser His Gln Arg Arg Arg Ala Thr Gly
      195      200      205
Lys Gln Gly Ser Arg Thr Ala Pro Val Gly Pro Lys Ser Tyr Ser Thr
      210      215      220
Pro Ala Glu Pro Glu Pro Gln Ser Ser Ala Ser Gln Ser Ser Gly Ala
      225      230      235      240
Ser Glu Ala Asp Ser Pro His Gln Lys Arg Pro Arg Arg Gln Val Thr
      245      250      255
Gln Lys Thr Val Val Val Lys Glu Glu Asp Pro Gly Glu Ile Gln Val
      260      265      270
Lys Glu Glu Pro Gln Glu Thr Ala Ile Ser Thr Pro Gly Lys Arg Lys
      275      280      285
Arg Asp Pro Ala Glu Gly Glu Thr Gln Gly Asn Pro Thr Arg Ser Arg
      290      295      300

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Arg Thr Lys Pro Asn Gln Glu Ala Ala Ala Pro Lys Val Leu Phe Thr
305          310          315          320
Gly Val Val Asp Ser Arg Gly Glu Arg Ala Val Leu Ala Leu Gly Gly
          325          330          335
Ser Leu Ala Ser Ser Val Asn Glu Ala Ser His Leu Val Thr Asp Arg
          340          345          350
Ile Arg Arg Thr Val Lys Phe Leu Cys Ala Val Gly Lys Gly Ile Pro
          355          360          365
Ile Leu Ser Leu Asn Trp Leu Tyr Gln Ser Arg Lys Ala Gly Cys Phe
          370          375          380
Leu Pro Pro Asp Asp Tyr Leu Val Thr Asp Pro Glu Gln Glu Lys Asn
385          390          395          400
Phe Ser Phe Ser Leu Arg Asp Ser Leu Ser Arg Ala Arg Glu Arg Arg
          405          410          415
Leu Leu Glu Asp Tyr Glu Ile His Val Thr Pro Gly Val Gln Pro Pro
          420          425          430
Pro Pro Gln Met Gly Glu Ile Ile Ser Cys Cys Gly Gly Thr Val Leu
          435          440          445
Pro Ser Met Pro His Ser Tyr Lys Leu His Arg Val Val Ile Thr Cys
          450          455          460
Thr Glu Asp Leu Pro Arg Cys Ala Ile Ala Ser Arg Leu Gly Leu Pro
465          470          475          480
Leu Leu Ser Pro Glu Phe Leu Leu Thr Gly Val Leu Lys Gln Glu Ala
          485          490          495
Thr Pro Glu Ala Trp Ser Ser Pro Ile Trp Lys Cys Ser Leu Pro Lys
          500          505          510
Lys Lys Lys Lys
          515

```

```

<210> 663
<211> 747
<212> PRT
<213> Rat

```

```

<400> 663
Glu Ala Thr Val Ile Thr Thr Glu Lys Arg Glu Arg Pro Ala Pro Pro
1          5          10          15
Arg Glu Leu Leu Val Pro Gln Ala Glu Val Thr Ala Arg Ser Leu Arg
          20          25          30
Leu Gln Trp Val Pro Gly Ser Asp Gly Ala Ser Pro Ile Arg Tyr Phe
          35          40          45
Thr Val Gln Val Arg Glu Leu Pro Gly Gly Glu Trp Gln Thr Tyr Ser
          50          55          60
Ser Ser Ile Ser His Glu Ala Thr Leu Cys Ala Val Glu Arg Leu Arg
65          70          75          80
Pro Phe Thr Ser Tyr Lys Leu Arg Leu Lys Ala Thr Asn Asp Ile Gly
          85          90          95
Asp Ser Asp Phe Ser Ala Glu Thr Glu Ala Val Thr Thr Leu Gln Asp
          100          105          110
Val Pro Gly Glu Pro Pro Gly Ser Val Ser Ala Thr Pro His Thr Thr
          115          120          125
Ser Ser Val Leu Ile Gln Trp Gln Pro Pro Arg Asp Glu Ser Leu Asn
          130          135          140
Gly Leu Leu Gln Gly Tyr Arg Ile Tyr Tyr Arg Glu Leu Glu Ser Glu
145          150          155          160
Thr Gly Leu Ser Pro Glu Pro Lys Thr Leu Lys Ser Pro Ser Ala Leu
          165          170          175

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Arg Ala Glu Leu Thr Ala Gln Ser Ser Phe Lys Thr Val Asn Ser Ser  
 180 185  
 Ser Thr Leu Thr Thr Tyr Glu Leu Thr His Leu Lys Lys Tyr Arg Arg  
 195 200 205  
 Tyr Glu Val Ile Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro Ala  
 210 215 220  
 Ser Val Pro Val Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met Ala  
 225 230 235 240  
 Pro Gln Asn Ile Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu Val  
 245 250 255  
 Thr Trp Asp Pro Pro Pro Glu Ser Gln Asn Gly Asn Ile Gln Gly  
 260 265 270  
 Tyr Lys Val Tyr Tyr Trp Glu Ala Asp Ser Arg Asn Glu Thr Glu Lys  
 275 280 285  
 Met Lys Val Leu Phe Leu Pro Glu Pro Val Val Lys Ile Lys Asp Leu  
 290 295 300  
 Thr Ser His Thr Lys Tyr Leu Val Ser Ile Ser Ala Phe Asn Ala Ala  
 305 310 315 320  
 Gly Asp Gly Pro Arg Ser Asp Pro Cys Gln Gly Arg Thr His Gln Ala  
 325 330 335  
 Ala Pro Gly Pro Pro Ser Phe Leu Glu Phe Ser Glu Ile Thr Ser Thr  
 340 345 350  
 Thr Leu Asn Val Ser Trp Gly Glu Pro Ser Ala Ala Asn Gly Ile Leu  
 355 360 365  
 Gln Gly Tyr Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly Val  
 370 375 380  
 Ser Lys Val Val Thr Val Asp Val Lys Gly Asn Trp Gln Arg Trp Leu  
 385 390 395 400  
 Lys Val Arg Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val Gln  
 405 410 415  
 Ala Arg Thr Ile Ala Tyr Gly Pro Glu Leu Gln Ala Asn Val Thr Ala  
 420 425 430  
 Gly Pro Ala Glu Gly Ser Pro Gly Ser Pro Arg Asn Val Leu Val Thr  
 435 440 445  
 Lys Ser Ala Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly Asn Thr Gly  
 450 455 460  
 Asn Thr Pro Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp Glu  
 465 470 475 480  
 Gly Leu Trp Asp Met Phe Ala Lys Asp Ile Pro Arg Ser Ala Thr Ser  
 485 490 495  
 Tyr Thr Val Gly Leu Asp Lys Leu Arg Gln Gly Val Thr Tyr Glu Phe  
 500 505 510  
 Arg Val Val Ala Val Asn Lys Ala Gly Phe Gly Glu Pro Ser Arg Pro  
 515 520 525  
 Ser Ile Ala Val Ser Ala Gln Ala Glu Ala Pro Phe Tyr Glu Glu Trp  
 530 535 540  
 Trp Phe Leu Leu Val Ile Ala Leu Ser Ser Leu Leu Leu Val Leu Leu  
 545 550 555 560  
 Val Val Phe Val Leu Val Leu His Gly Gln Ser Lys Lys Tyr Lys Asn  
 565 570 575  
 Cys Gly Ser Gly Lys Gly Ile Ser Asn Met Glu Glu Thr Val Thr Leu  
 580 585 590  
 Asp Asn Gly Gly Phe Ala Ala Leu Glu Leu Asn Ser Arg His Leu Asn  
 595 600 605  
 Val Lys Ser Thr Phe Ser Lys Lys Asn Gly Thr Arg Ser Pro Pro Arg  
 610 615 620  
 Pro Ser Pro Gly Gly Leu His Tyr Ser Asp Glu Asp Ile Cys Asn Lys

```

625          630          635          640
Tyr Asn Gly Ala Val Leu Thr Glu Ser Val Asn Leu Lys Glu Lys Ser
645          650          655
Val Asp Gly Ser Glu Ser Glu Ala Ser Asp Ser Asp Tyr Glu Glu Ala
660          665          670
Leu Pro Lys His Ser Phe Val Asn His Tyr Met Ser Asp Pro Thr Tyr
675          680          685
Tyr Asn Phe Trp Lys Arg Arg Pro Pro Ala Ala Ala Pro His Arg Tyr
690          695          700
Glu Ala Val Ala Gly Ala Glu Ala Gly Pro His Leu His Thr Val Ile
705          710          715          720
Thr Thr Gln Ser Ala Gly Gly Val Tyr Thr Pro Ala Gly Pro Gly Ala
725          730          735
Arg Ala Pro Leu Thr Gly Phe Ser Ser Phe Val
740          745

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&lt;210&gt; 664

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 664

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Met Gln Leu Asn Arg Phe Phe Ser Gly Pro Gly Leu Phe Leu Leu Leu
1          5          10          15
Phe Cys Ser Leu Cys Val Glu Ala Glu Val Lys Glu Val Asn Ala Met
20          25          30
Val Gly Ser Asp Val Glu Leu Arg Cys Val Tyr Pro Arg Arg Ser His
35          40          45
Phe Ser Leu Asp Asp Leu Tyr Val Tyr Trp Gln Ile Val Asp Glu Ala
50          55          60
Lys Thr Val Val Thr Tyr Tyr Leu Pro Ser Ala Asn Glu Ser Ser Thr
65          70          75          80
Ile His Val Ser Asn Ser Tyr Lys Asn Arg Ala His Leu Ser Pro Asp
85          90          95
Leu Met Lys Glu Gly Asp Phe Ser Leu His Leu Gln Asn Val Thr Pro
100          105          110
Gln Asp Thr Gln Glu Phe Lys Cys Leu Val Phe Arg Met Ser Thr Val
115          120          125
Leu Gly Lys Ala Leu Glu Glu Val Val Arg Leu Arg Val Ala Ala Asn
130          135          140
Phe Ser Thr Pro Val Ile Ser Thr Ser Gly Ser Ser Asp Pro Gly Gln
145          150          155          160
Glu Arg Thr Phe Thr Cys Met Ser Lys Asn Gly Tyr Pro Glu Pro Asn
165          170          175
Leu Tyr Trp Ile Asn Arg Thr Asp Asn Thr Leu Ile Asp Glu Thr Leu
180          185          190
Gln Asn Asn Thr Val Tyr Leu Asn Glu Leu Gly Leu Tyr Asp Val Val
195          200          205
Ser Thr Leu Arg Ile Pro Trp Thr Pro His Val Asp Val Ile Cys Cys
210          215          220
Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile Ser Arg Ala
225          230          235          240
Asp Ser Phe Thr Gly Ser Met Asn Thr Glu Arg Pro Gln Glu Ile His
245          250          255
Arg Glu Ala Thr Lys Val Leu Phe Tyr Ala Leu Ala Ala Leu Leu Ala
260          265          270
Val Val Val Val Ile Phe Ile Ile Val Leu Tyr Arg Cys Arg Arg Arg

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275                      280                      285  
 Pro Cys Gln Ser Tyr Thr Gly Pro Arg Ala Val Gln Leu Glu Leu Thr  
 290                      295                      300  
 Asp His Ser  
 305

<210> 665  
 <211> 143  
 <212> PRT  
 <213> Rat

<400> 665  
 Lys Lys Tyr Asp Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Val  
 1                      5                      10                      15  
 Val Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Thr Gly Val  
 20                      25                      30  
 Thr Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg  
 35                      40                      45  
 His Thr Gly Met His Asn Ser Ala Phe Ser Gly Phe Met Leu Gly Pro  
 50                      55                      60  
 Phe Phe Trp Leu Leu Phe Lys Ser Pro Gln Leu Ala Ala Gln Pro Ser  
 65                      70                      75                      80  
 Thr Tyr Leu Ala Val Ala Glu Glu Leu Glu Ser Val Ser Gly Lys Tyr  
 85                      90                      95  
 Phe Asp Gly Leu Arg Glu Lys Ala Pro Ser Pro Glu Ala Glu Asp Glu  
 100                      105                      110  
 Glu Val Ala Arg Arg Leu Trp Thr Glu Ser Ala His Leu Val Gly Leu  
 115                      120                      125  
 Asp Met Ala His Gly Ser Ser Gly Arg Gly His Ser Ile Ser Arg  
 130                      135                      140

<210> 666  
 <211> 298  
 <212> PRT  
 <213> Mouse

<400> 666  
 Met Glu Ser Ala Asn Thr Leu Cys Pro Gly Arg Lys Cys Lys Gly Gly  
 1                      5                      10                      15  
 Val Leu Ala His Leu Glu Arg Leu Glu Ala Gln Thr Asn Ile Ser Asn  
 20                      25                      30  
 Arg Lys Ser Glu Glu Pro Ala Val Arg Lys Lys Glu Ser Ser Leu Arg  
 35                      40                      45  
 Thr Lys Ile Arg Glu Leu Arg Gln Gln Arg Asp Lys Leu Arg Ala Glu  
 50                      55                      60  
 Val Lys Gln Trp Gly Ala Arg Val Lys Glu Pro Pro Ala Lys Glu Asp  
 65                      70                      75                      80  
 Pro Ser Arg Thr Val Ile Ser Glu Gln Glu Val Leu Glu Arg Glu Trp  
 85                      90                      95  
 Arg Asn Val Asp Ala Ile Leu Glu Ala Tyr Arg Phe Thr Gly Leu Ser  
 100                      105                      110  
 Gly Lys Leu Thr Ser Arg Gly Val Cys Met Cys Ile Ser Thr Ala Phe  
 115                      120                      125  
 Glu Gly Asn Leu Leu Asp Ser Tyr Phe Val Asp Leu Val Ile Glu Lys  
 130                      135                      140  
 Pro Leu Arg Ile His His Ser Val Pro Val Phe Ile Pro Leu Glu  
 145                      150                      155                      160

Lys Ile Ala Ala Ala His Leu Gln Thr Asp Val Gln Arg Phe Leu Phe  
 165 170 175  
 Arg Leu Trp Glu Tyr Leu Asn Ala Tyr Ala Gly Arg Lys Tyr Gln Ala  
 180 185 190  
 Asp Gln Leu Glu Ser Asp Phe Cys Asp Val Leu Thr Gly Pro Leu Gln  
 195 200 205  
 Arg Asn Ala Leu Cys Asn Leu Leu Ser Phe Thr Tyr Lys Val Glu Gln  
 210 215 220  
 Arg Cys Gln Thr Phe Ser Phe Ser Ala Arg Leu Leu Tyr Glu Asp Pro  
 225 230 235 240  
 Thr Ala Ala Leu Pro Thr Asn Val Thr Val Thr Arg Pro Gly Val Glu  
 245 250 255  
 Ala Ser Ser Pro Pro Trp Glu Glu His Arg Ala Ser His Gln Met Leu  
 260 265 270  
 Phe Arg Thr Lys Pro Leu His Lys Val Phe Ala Ser Phe Ser Lys Glu  
 275 280 285  
 Thr Glu Lys Leu His Leu Asn Leu Val Ser  
 290 295

<210> 667  
 <211> 226  
 <212> PRT.  
 <213> Mouse

<400> 667  
 Met Glu Ala Glu Leu Gly Gly Ser Phe Ile Lys Leu Arg Gln Ala Leu  
 1 5 10 15  
 Phe Gln Leu Asn Ser Val Asp Ser Ser Leu Leu Phe Thr Ala Gln Ala  
 20 25 30  
 Leu Leu Arg Trp His Asp Gly His Gln Phe Cys Ser Lys Ser Gly Gln  
 35 40 45  
 Pro Thr Gln Lys Asn Val Ala Gly Ser Lys Arg Val Cys Pro Ser Ser  
 50 55 60  
 Lys Ile Ile Tyr Tyr Pro Gln Met Ala Pro Val Val Ile Thr Leu Val  
 65 70 75 80  
 Ser Asp Gly Ala Arg Cys Leu Leu Ala Arg Gln Ser Ser Phe Pro Lys  
 85 90 95  
 Gly Leu Tyr Ser Ala Leu Ala Gly Phe Cys Asp Ile Gly Glu Ser Val  
 100 105 110  
 Glu Glu Thr Val His Arg Glu Val Ala Glu Glu Val Gly Leu Glu Val  
 115 120 125  
 Glu Asn Ile Gln Tyr Ser Ala Ser Gln His Trp Pro Phe Pro Asn Ser  
 130 135 140  
 Ser Leu Met Ile Ala Cys His Ala Thr Val Lys Pro Gly His Thr Glu  
 145 150 155 160  
 Ile Gln Val Asn Leu Lys Glu Leu Glu Ala Ala Ala Trp Phe Ser Leu  
 165 170 175  
 Asp Glu Val Thr Thr Ala Leu Arg Arg Lys Gly Ser Leu Ala Leu Gln  
 180 185 190  
 Pro Ser Glu Ala Ser Pro Leu Leu Leu Pro Pro Lys Leu Ala Ile Ala  
 195 200 205  
 His His Leu Ile Lys Lys Trp Val Glu Thr Arg Ser Cys Ser Ser Leu  
 210 215 220  
 Ala Ala  
 225

<210> 668

<211> 781  
 <212> PRT  
 <213> Mouse

<400> 668

```

Met Glu Met Met Lys Lys Leu Ile Ala Gly Gln Gly Pro Glu Pro Gln
 1      5      10      15
Pro Ser Asn Arg Pro Thr Ser Arg Leu Gly Gly Ser Leu Leu Phe Gly
      20      25      30
Asn Leu Val Pro Ala Asn Lys Asp Ala Pro Ala Leu Glu Pro Leu Gly
      35      40      45
Thr Lys Leu Ser Ala Leu Pro Pro His Gly Ala Pro Gly Val Arg Lys
      50      55      60
Val Pro Gly Gln Leu Pro Leu Leu Cys Ser Gly Arg Pro Pro Pro Glu
65      70      75      80
Lys Pro Ala Pro Ile Glu Pro Pro Glu Gly Trp Ser Pro Ala Pro Lys
      85      90      95
Thr Gln Gly Lys Leu Asn Thr Arg Pro Gly Lys Val Ile Leu Phe Ser
      100      105      110
Glu Pro Gly Cys Arg Gly Arg Gly Arg Glu Val Trp Gly Asp Ile Ala
      115      120      125
Asp Ala Ser Ala Trp Asp Pro Val Ala Ser Ile Arg Val Ile Arg Gly
130      135      140
Cys Trp Ile Leu Tyr Glu Gln Pro Glu Phe Arg Gly Gln Lys Leu Ser
145      150      155      160
Leu Pro Glu Gly Asp Val Glu Leu Arg Ala Leu Ala Cys Ala Trp Ser
      165      170      175
Leu Gln Gly Phe Gly Ser Leu Arg Arg Ala Val Gln Asp Tyr Cys Thr
      180      185      190
Pro Thr Ile Ser Leu Phe Ser Glu Glu Gly Leu Lys Gly Lys Pro Val
195      200      205
Thr Leu Thr Gly Asp Leu Lys Asp Ser Gln Gly Leu Glu Arg Pro Leu
210      215      220
Gln Val Ala Ser Ala Thr Val Thr Ala Gly Leu Trp Leu Leu Tyr Pro
225      230      235      240
Lys Pro Phe Phe Glu Asp Thr Pro Tyr Ile Leu Glu Pro Gly Glu Tyr
      245      250      255
Pro Thr Leu Glu Ala Trp Gly Thr Ser Gly Pro Ser Val Gly Ser Leu
260      265      270
Lys Pro Met Arg Leu Gly Cys Pro Ser Val Glu Lys Pro Gly Glu Pro
275      280      285
Lys Ala Val Val Tyr Glu Ala Pro Gly Phe Gln Gly Gln Ser Trp Glu
290      295      300
Val Ser Gly Asp Ile Tyr Asn Leu Gln Gln Pro Glu Asp Ser Gln Ser
305      310      315      320
Pro Gln Leu Thr Ser Val Gly Ser Leu Arg Ile Leu Gly Gly Cys Trp
      325      330      335
Val Gly Tyr Glu Lys Glu Gly Phe Arg Gly His Gln Tyr Leu Leu Glu
      340      345      350
Glu Gly Glu Tyr Ala Asp Trp Ser His Trp Gly Gly Tyr Asp Glu Leu
355      360      365
Leu Thr Ser Leu Arg Val Ile Arg Thr Asp Phe Gly Asp Pro Ala Val
370      375      380
Val Leu Phe Glu Asp Met Asp Phe Gln Gly His Arg Val Glu Val Ser
385      390      395      400
Ser Ala Leu Pro Asp Val Glu Leu Ala Gln His Gly Pro Ser Thr Gln
      405      410      415

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Ala Ile His Val Leu Ser Gly Val Trp Val Ala Tyr Glu Arg Val Gly  
 420 425 430  
 Phe Ser Gly Glu Gln Tyr Ile Leu Glu Lys Gly Val Tyr Arg Asn Cys  
 435 440 445  
 Asp Asp Trp Gly Ser Gly Asn Cys Ala Leu Gly Ser Leu Gln Pro Val  
 450 455 460  
 Val Gln Val Gly Glu Ser Asp Leu His Phe Val Thr Lys Ile Gln Leu  
 465 470 475 480  
 Phe Ser Gly Pro Asn Phe Leu Gly Asp His Ile Ser Phe Glu Asp Asp  
 485 490 495  
 Gln Ala Ser Leu Pro Ala Ser Phe His Pro Gln Ser Cys Arg Val His  
 500 505 510  
 Gly Gly Ser Trp Val Leu Phe Glu Asp Lys Asn Phe Glu Ala Asp Gln  
 515 520 525  
 His Ile Val Ser Glu Gly Glu Phe Pro Thr Leu Thr Asp Met Gly Cys  
 530 535 540  
 Leu Ala Ser Thr Val Leu Gly Ser Leu Arg Lys Val Pro Leu His Phe  
 545 550 555 560  
 Ser Glu Pro Ser Leu Ser Leu Phe Gly Leu Glu Cys Phe Glu Gly Lys  
 565 570 575  
 Glu Ile Glu Leu Thr Gly Glu Val Arg Ser Leu Gln Ala Glu Gly Phe  
 580 585 590  
 Asn Asn His Val Leu Ser Val Arg Val Lys Gly Gly Val Trp Val Val  
 595 600 605  
 Cys Glu His Ser Asp Phe Arg Gly Arg Gln Trp Leu Val Gly Ser Cys  
 610 615 620  
 Glu Ile Thr Asn Trp Leu Thr Tyr Ser Gly Thr Gln Arg Val Gly Ser  
 625 630 635 640  
 Leu Tyr Pro Ile Lys Gln Arg Arg Ala Tyr Phe Arg Leu Trp Asn Ala  
 645 650 655  
 Ala Leu Gly Gly Phe Leu Ser Val Pro Asp His Val Glu Asp Met Lys  
 660 665 670  
 Ala Gly Arg Val Val Val Ser Glu Pro Arg Ala Gly Gly Ser Cys Ile  
 675 680 685  
 Trp Tyr Tyr Glu Asp Gly Leu Leu Lys Asn Gln Met Ala Pro Thr Met  
 690 695 700  
 Ser Leu Gln Val Ile Gly Pro Pro Ser Pro Gly Ser Lys Val Val Leu  
 705 710 715 720  
 Trp Ala Glu Ser Arg Leu Pro Arg Gln Thr Trp Ser Ile Asn Glu Leu  
 725 730 735  
 Gly His Ile Cys Ser Gln Met Phe Glu Gly Gln Ile Leu Asp Val Lys  
 740 745 750  
 Gly Gly Arg Gly Tyr Asp Arg Asp His Val Val Leu Trp Glu Pro Thr  
 755 760 765  
 Lys Asp Arg Leu Ser Gln Ile Trp Thr Val His Val Leu  
 770 775 780

&lt;210&gt; 669

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 669

Met Tyr Met Thr Met Arg Gly Lys Glu Pro Trp Gln Thr Ala Lys Leu  
 1 5 10 15  
 Gln Leu Gly Glu Leu Asn Arg Thr Ala Val Phe Thr Cys Arg Pro Ala  
 20 25 30

Arg Val Lys Glu Gly Asp Ile Leu Tyr Ile His Ser Leu Gln Thr Val  
           35                  40                  45  
 Gly Ser Asn His Lys Pro Val Ala Ala Glu His Thr Tyr Trp Ala Trp  
           50                  55                  60  
 Pro Glu Glu Thr Asp Val  
           65                  70

<210> 670  
 <211> 368  
 <212> PRT  
 <213> Mouse

<400> 670  
 Leu Thr Asn Gly Ser Gln Ala Ser Asp Lys Ser Glu Glu Gly Ser Ala  
   1                  5                  10                  15  
 Asp Thr Ala Asp Pro Gln Glu Asn Pro Leu Gln Pro Val Ser Val Gly  
           20                  25                  30  
 Glu Glu Pro Ser Ile Thr Glu His Ser Val Gly Glu Gln Ala Trp  
           35                  40                  45  
 Asp Gly Thr Ser Gln Ser Cys Pro Ser Leu Pro Ala Thr Val Ser Phe  
           50                  55                  60  
 His Met Asp Ser Thr Asp Leu Glu Pro Gly Gln Gln Thr Ala Met Lys  
           65                  70                  75                  80  
 Ser Cys Ser Arg Asp Asp Val Glu Met Val Glu Glu Phe Asp Glu Leu  
                   85                  90                  95  
 Pro Thr Asp Ala Val Arg Arg Ile Arg Arg Glu Leu Val Thr Val Thr  
           100                  105                  110  
 Lys His Ser Pro Glu Gln Arg Gln Asp Pro Leu Cys Ile Ser Ile Thr  
           115                  120                  125  
 Val Cys Thr Val Glu Lys Asp Arg Pro Ala Ala Leu Asp Ser Leu Glu  
           130                  135                  140  
 Glu Pro Leu Pro Gly Met Leu Phe Phe Leu Ser Ser Gly Gln Asp Gln  
           145                  150                  155                  160  
 Gln Ala His Pro Gln Leu Arg Glu His Pro Ala Pro Glu Ala Ser Glu  
                   165                  170                  175  
 Ala Ser Gln Pro Gln Asp Ala Ala Glu Gly Ser Ser Ala Gly Glu Glu  
           180                  185                  190  
 Lys Asp Ala Ser Val Glu Pro Leu Leu Pro Ala Ala Ser Pro Gly Gly  
           195                  200                  205  
 Ser Thr Ser Gln Val Leu Glu Ala Ala Thr Cys Lys Lys Gln Val Ser  
           210                  215                  220  
 Gln Asp Phe Leu Glu Thr Arg Phe Lys Ile Gln Gln Leu Leu Glu Pro  
           225                  230                  235                  240  
 Gln Gln Tyr Met Ala Cys Leu Pro His His Ile Ile Val Lys Ile Phe  
                   245                  250                  255  
 Arg Leu Leu Pro Thr Leu Ser Leu Ala Ile Leu Lys Cys Thr Cys Arg  
           260                  265                  270  
 Tyr Phe Lys Ser Ile Ile Glu Tyr Tyr Asn Ile Arg Pro Ala Asp Ser  
           275                  280                  285  
 Arg Trp Val Arg Asp Pro Arg Tyr Arg Glu Asp Pro Cys Lys Gln Cys  
           290                  295                  300  
 Lys Lys Lys Tyr Val Lys Gly Asp Val Ser Leu Cys Arg Trp His Pro  
           305                  310                  315                  320  
 Lys Pro Tyr Cys Gln Ala Leu Pro Tyr Gly Pro Gly Tyr Trp Met Cys  
                   325                  330                  335  
 Cys Pro Pro Val Ser Glu Gly Leu Phe Cys Cys Lys Leu Gly Leu His  
           340                  345                  350



Asp Asn His Trp Leu Pro Ala Cys His Ser Phe Asn Pro Gly Asn Pro  
 355 360 365

<210> 671  
 <211> 293  
 <212> PRT  
 <213> Mouse

<400> 671  
 Thr His Phe Ile His Thr Leu Thr Arg Leu Gln Met Glu Gln Gly Ala  
 1 5 10 15  
 Glu Ser Leu Gly Asp Leu Glu Ser Pro Val Glu Asp Thr Pro Val Glu  
 20 25 30  
 Gln Ala Ala Leu Ser Pro Phe Pro Ser Lys Pro Pro Val Ser Ser  
 35 40 45  
 Glu Leu Gly Asp Ser Ser Cys Ser Ser Asp Met Thr Asp Ser Ser Thr  
 50 55 60  
 Thr Leu Ser Ser Gly Ser Ser Glu Pro Pro Asn His Pro Ala His Pro  
 65 70 75 80  
 Ser Leu Pro Gly Pro Ser Phe Arg Ser Gly Val Asp Glu Asp Ser Leu  
 85 90 95  
 Glu Gln Ile Leu Asn Phe Ser Asp Ser Asp Leu Gly Ile Glu Glu  
 100 105 110  
 Glu Glu Glu Gly Gly Gly Val Gly Asn Ser Asp Asn Leu Ser Cys Phe  
 115 120 125  
 His Leu Ala Asp Ile Phe Gly Thr Gly Asp Pro Gly Ser Leu Ala Ser  
 130 135 140  
 Trp Thr His Ser Gln Ser Gly Ser Ser Leu Ala Ser Gly Ile Leu Asp  
 145 150 155 160  
 Glu Asn Ala Asn Leu Asp Ala Ser Cys Phe Leu Asn Ser Gly Leu Gly  
 165 170 175  
 Gly Leu Arg Glu Gly Ser Leu Pro Gly Ser Ser Gly Ser Pro Glu Gly  
 180 185 190  
 Asp Ala Val Gln Ser Ser Ser Trp Asp Leu Ser Leu Ser Ser Cys Asp  
 195 200 205  
 Ser Phe Glu Leu Leu Gln Ala Leu Pro Asp Tyr Ser Leu Gly Pro His  
 210 215 220  
 Tyr Thr Ser Arg Arg Val Ser Gly Ser Pro Asp Ser Leu Glu Thr Phe  
 225 230 235 240  
 His Pro Leu Pro Ser Phe Ser Pro Pro Arg Asp Ala Ser Thr Cys Phe  
 245 250 255  
 Leu Glu Ser Leu Val Gly Leu Ser Glu Pro Val Thr Glu Val Leu Ala  
 260 265 270  
 Pro Leu Leu Glu Ser Gln Phe Glu Asp Ala Ala Leu Ala Pro Leu Leu  
 275 280 285  
 Glu Pro Val Pro Val  
 290

<210> 672  
 <211> 904  
 <212> PRT  
 <213> Mouse

<400> 672  
 Met Glu Val Asn Cys Leu Thr Leu Lys Asp Leu Ile Ser Pro Arg Gln  
 1 5 10 15  
 Thr Arg Leu Asp Phe Ala Ile Glu Asp Ala Glu Asn Ala Gln Lys Glu

		20				25				30			
Asn	Ile	Phe	Val	Asp	Arg	Ser	Arg	Met	Thr	Pro	Lys	Thr	Pro
		35					40					45	Met
Asn	Glu	Pro	Ile	Asp	Leu	Ser	Lys	Gln	Arg	Ile	Phe	Thr	Pro
		50				55					60		Asp
Asn	Pro	Ile	Thr	Pro	Val	Lys	Pro	Val	Asp	Arg	Gln	Pro	Gln
65					70				75				80
Pro	Trp	Thr	Pro	Thr	Ala	Asn	Leu	Lys	Met	Leu	Ile	Ser	Ala
				85					90				95
Pro	Asp	Ile	Arg	Asp	Arg	Glu	Lys	Lys	Lys	Glu	Leu	Phe	Arg
			100					105					110
Glu	Asn	Lys	Glu	Asp	Ala	Phe	Val	Asn	Ser	Leu	Gln	Leu	Asp
		115					120					125	Val
Gly	Asp	Gly	Ala	Val	Asp	Glu	Tyr	Glu	Lys	Gln	Arg	Pro	Ser
130						135					140		Arg
Gln	Lys	Ser	Leu	Gly	Leu	Leu	Cys	Gln	Lys	Phe	Leu	Ala	Arg
145					150					155			Tyr
Ser	Tyr	Pro	Leu	Ser	Thr	Glu	Lys	Thr	Thr	Ile	Ser	Leu	Asp
			165					170					175
Ala	Val	Ser	Leu	Gly	Val	Glu	Arg	Arg	Arg	Ile	Tyr	Asp	Ile
			180					185					190
Val	Leu	Glu	Ser	Leu	His	Leu	Val	Ser	Arg	Val	Ala	Lys	Asn
		195					200					205	Gln
Gly	Trp	His	Gly	Arg	His	Ser	Leu	Pro	Lys	Thr	Leu	Arg	Thr
210					215						220		Leu
Arg	Leu	Gly	Glu	Glu	Gln	Lys	Tyr	Glu	Glu	Gln	Met	Ala	Cys
225					230					235			Leu
Gln	Lys	Glu	Leu	Asp	Leu	Met	Gly	Tyr	Arg	Phe	Gly	Glu	Arg
			245						250				Arg
Asp	Gly	Ser	Pro	Asp	Pro	Arg	Asp	Pro	His	Leu	Leu	Asp	Phe
			260					265					270
Ala	Asp	Tyr	Pro	Ser	Ser	Ser	Ala	Asn	Ser	Arg	Lys	Asp	Lys
		275					280					285	Ser
Arg	Ile	Met	Ser	Gln	Lys	Phe	Val	Met	Leu	Phe	Leu	Val	Ser
290						295					300		Lys
Lys	Ile	Val	Thr	Leu	Asp	Val	Ala	Ala	Lys	Ile	Leu	Ile	Glu
305					310					315			Glu
Gln	Asp	Thr	Pro	Asp	His	Ser	Lys	Phe	Lys	Thr	Lys	Val	Arg
			325						330				Arg
Tyr	Asp	Ile	Ala	Asn	Val	Leu	Thr	Ser	Leu	Ala	Leu	Ile	Lys
			340					345					Lys
His	Val	Thr	Glu	Glu	Arg	Gly	Arg	Lys	Pro	Ala	Phe	Lys	Trp
		355					360					365	Ile
Pro	Val	Asp	Phe	Ser	Ser	Ile	Asp	Glu	Glu	Leu	Leu	Asp	Val
		370					375					380	Ser
Ser	Ile	Leu	Pro	Glu	Leu	Lys	Lys	Glu	Ala	Tyr	Gly	Gln	Ile
385					390					395			Arg
Cys	Ala	Lys	Glu	Arg	Leu	Val	Arg	Tyr	Gly	Ser	Phe	Asn	Thr
			405						410				Val
Thr	Ser	Glu	Lys	Ile	Gln	Arg	Lys	Val	Ser	Ser	Glu	Pro	Ser
		420						425				430	Ser
Gln	Gly	Glu	Arg	Gln	Gly	Ser	Ala	Tyr	Ser	Leu	Glu	Ile	Gly
		435					440					445	Ser
Ala	Ala	Ile	Tyr	Arg	Gln	Lys	Val	Glu	Asp	Asn	Ser	Gln	Glu
		450				455					460		Ala
Phe	Val	Ser	Asn	Thr	Ala	Val	Pro	Pro	Ala	Ser	Ile	Leu	Asp
465					470					475			Pro
													Ala

Leu Ser Met Asp Ser Glu Tyr Cys Val Lys Pro Leu Ala Gln Pro Val  
 485 490 495  
 Phe Ser Val Ala Gln Thr Asp Leu Pro Ala Phe Ser Ala Gln Asn Gly  
 500 505 510  
 Pro Ser Gly Gln Val Gly Val Pro Val Pro Ser Ala Ala Ser Asp Thr  
 515 520 525  
 Glu Asn Leu Lys Pro Ala Leu Leu Ala Gly Gln Pro Leu Val Tyr Val  
 530 535 540  
 Pro Ser Thr Gln Leu Phe Met Leu Tyr Gly Ser Val Gln Glu Gly Leu  
 545 550 555 560  
 Ser Pro Glu Ser Arg Ser Glu Glu Asp Gly Gly Gly Ser Asp Val Pro  
 565 570 575  
 Ala Asp Leu Ser Val Thr Pro Ser Ala Gln Lys Arg Leu Cys Glu Glu  
 580 585 590  
 Arg Asp Pro Gln Glu Glu Glu Asp Glu Pro Ala Met Lys Arg Gln Ser  
 595 600 605  
 Gln Glu Phe Glu Asp Ser Pro Leu Ser Leu Val Met Pro Lys Lys Pro  
 610 615 620  
 Ser Ser Ser Thr Asp Leu Ala Cys Pro Val Thr Met Gly Asn Gly Ser  
 625 630 635 640  
 Ser Pro Pro Leu Glu Asp Ala Cys Val Lys Gly Gln Leu Pro Ala Ala  
 645 650 655  
 Glu Glu Val Thr Gly Lys Ala Ala Pro Asn Cys Tyr Val Ala Ser Glu  
 660 665 670  
 Cys Gly Asn Pro Ala Arg Asn Pro Asp Thr Glu Lys Pro Ser Asn Glu  
 675 680 685  
 Asn Glu Ile Thr Lys Asp Pro Ser Leu Met Gln Tyr Leu Tyr Val Gln  
 690 695 700  
 Ser Pro Ala Gly Leu Asn Gly Phe Asn Met Val Leu Pro Gly Thr Gln  
 705 710 715 720  
 Thr Pro His Thr Val Ala Pro Ser Pro Ala Gln Leu Pro Ser Phe Gly  
 725 730 735  
 Val Pro Cys Met Phe Leu Gln Ser Pro Gly Leu Gly Pro Phe Pro Val  
 740 745 750  
 Leu Tyr Ser Pro Ala Ile Pro Gly Pro Ile Ser Ser Ala Pro Gly Thr  
 755 760 765  
 His Pro Asn Pro Gly Pro Met Asn Phe Gly Leu Ser Thr Leu Ala Ser  
 770 775 780  
 Ala Ser His Leu Leu Ile Ser Pro Ala Ala Met Val Asn Pro Lys Pro  
 785 790 795 800  
 Ser Thr Leu Pro Cys Thr Asp Pro Gln Leu Arg Cys Gln Pro Ser Leu  
 805 810 815  
 Asn Leu Asn Pro Val Met Pro Gly Ser His Gly Val Ile His Pro Glu  
 820 825 830  
 Ser Pro Cys Tyr Val Arg His Pro Val Ser Met Val Lys Ala Glu Gln  
 835 840 845  
 Ser Pro Ala Pro Ala Thr Pro Lys Ser Ile Gln Arg Arg His Arg Glu  
 850 855 860  
 Thr Phe Phe Lys Thr Pro Gly Ser Leu Gly Asp Pro Val Phe Arg Arg  
 865 870 875 880  
 Lys Glu Arg Asn Gln Ser Arg Asn Thr Ser Ser Ala Gln Arg Arg Leu  
 885 890 895  
 Glu Ile Ser Ser Ser Gly Pro Asp  
 900

&lt;210&gt; 673

&lt;211&gt; 173

<212> PRT  
<213> Mouse

<400> 673

```

Lys Arg Arg Lys Arg Lys Arg Ser Glu Gly Leu Ser Gln Glu Ala Thr
 1           5           10           15
Pro Ser Gln Asp Leu Ile Gln His Ser Cys Ser Pro Val Asp His Ser
 20           25           30
Glu Pro Glu Ala Arg Thr Glu Leu Gln Lys Lys Lys Lys Lys Arg
 35           40           45
Arg Lys Arg Lys Pro Glu Pro Gln Gln Asp Glu Glu Ser Lys His Pro
 50           55           60
Gly Asp Gln Arg Ser Pro Arg Pro Ser Val Thr Pro Val Pro Ala Leu
 65           70           75           80
Ser Val Asn Gly His Leu Pro Ser Asp Cys Leu Val Leu Thr Trp Asp
 85           90           95
Gly Glu Pro Ser Ala Ile Ser Gln Asp Ala Ile Lys Asp Ser Arg Leu
100           105           110
Ala Arg Thr Gln Thr Val Val Asp Asp Trp Asp Glu Glu Phe Asp Arg
115           120           125
Gly Lys Glu Lys Lys Ile Lys Lys Phe Lys Arg Glu Lys Lys Arg Asn
130           135           140
Phe Asn Ala Phe Gln Lys Leu Gln Ser Arg Arg Asn Phe Trp Ser Val
145           150           155           160
Thr His Pro Ala Lys Val Ala Ser Leu Ser Tyr Arg Arg
165           170

```

<210> 674  
<211> 470  
<212> PRT  
<213> Mouse

<400> 674

```

Glu Glu Thr Lys Pro Leu Leu Gly Ser Asp Val Ser Gly Pro Glu Gly
 1           5           10           15
Thr Lys Val Met Gly Ala Val Pro Cys Arg Arg Ala Leu Leu Leu Cys
 20           25           30
Asn Gly Met Arg Tyr Lys Leu Leu Gln Glu Gly Asp Ile Gln Val Cys
 35           40           45
Val Ile Arg His Pro Arg Thr Phe Leu Ser Lys Ile Leu Thr Ser Lys
 50           55           60
Phe Leu Arg Arg Trp Glu Pro His His Leu Thr Leu Ala Asp Asn Ser
 65           70           75           80
Leu Ala Ser Ala Thr Pro Ser Gly Tyr Met Glu Asn Ser Val Ser Tyr
 85           90           95
Ser Ala Ile Glu Asp Val Gln Pro Leu Ser Trp Glu Asn Ala Pro Lys
100           105           110
Tyr Cys Leu Gln Leu Thr Ile Pro Gly Gly Thr Val Leu Leu Gln Ala
115           120           125
Ala Asn Ser Tyr Leu Arg Asp Gln Trp Phe His Ser Leu Gln Trp Lys
130           135           140
Lys Lys Ile Tyr Lys Tyr Lys Lys Val Leu Ser Asn Pro Ser Arg Trp
145           150           155           160
Glu Val Val Leu Lys Glu Ile Arg Thr Leu Val Asp Met Ala Leu Thr
165           170           175
Ser Pro Leu Gln Asp Asp Ser Ile Asn Gln Ala Pro Leu Glu Ile Val
180           185           190

```

Ser Lys Leu Leu Ser Glu Asn Thr Asn Leu Thr Thr Gln Glu His Glu  
 195 200 205  
 Asn Ile Ile Val Ala Ile Ala Pro Leu Leu Glu Asn Asn His Pro Pro  
 210 215 220  
 Pro Asp Leu Cys Glu Phe Phe Cys Lys His Cys Arg Glu Arg Pro Arg  
 225 230 235 240  
 Ser Met Val Val Ile Glu Val Phe Thr Pro Val Val Gln Arg Ile Leu  
 245 250 255  
 Lys His Asn Met Asp Phe Gly Lys Cys Pro Arg Leu Arg Leu Phe Thr  
 260 265 270  
 Gln Glu Tyr Ile Leu Ala Leu Asn Glu Leu Asn Ala Gly Met Glu Val  
 275 280 285  
 Val Lys Lys Phe Ile Gln Ser Met His Gly Pro Thr Gly His Cys Pro  
 290 295 300  
 His Pro Arg Val Leu Pro Asn Leu Val Ala Val Cys Leu Ala Ala Ile  
 305 310 315 320  
 Tyr Ser Cys Tyr Glu Phe Ile Asn Ser Arg Asp Asn Ser Pro Ser  
 325 330 335  
 Leu Lys Glu Ile Arg Asn Gly Cys Gln Gln Pro Cys Asp Arg Lys Pro  
 340 345 350  
 Thr Leu Pro Leu Arg Leu Leu His Pro Ser Pro Asp Leu Val Ser Gln  
 355 360 365  
 Glu Ala Thr Leu Ser Glu Pro Arg Leu Lys Ser Val Val Val Ala Ser  
 370 375 380  
 Ser Glu Val His Val Glu Val Glu Arg Thr Ser Thr Ala Lys Pro Ala  
 385 390 395 400  
 Leu Thr Ala Ser Thr Gly Asn Asp Ser Glu Pro Asn Leu Ile Asp Cys  
 405 410 415  
 Leu Met Val Ser Pro Ala Cys Gly Thr Met Ser Ile Glu Leu Gly Pro  
 420 425 430  
 Gln Ala Gly Arg Thr Leu Gly Cys His Val Glu Ile Leu Lys Leu Leu  
 435 440 445  
 Ser Asp Tyr Asp Asp Trp Arg Pro Ser Leu Ala Ser Leu Leu Gln Pro  
 450 455 460  
 Ile Pro Phe Pro Lys Glu  
 465 470

<210> 675  
 <211> 319  
 <212> PRT  
 <213> Mouse

<400> 675  
 Phe Ala Arg Thr Leu Pro Trp Ala Ser Val Leu Arg Val Trp Asp Met  
 1 5 10 15  
 Phe Phe Cys Glu Gly Val Lys Ile Ile Phe Arg Val Ala Leu Val Leu  
 20 25 30  
 Leu Arg His Thr Leu Gly Ser Val Glu Lys Leu Arg Ser Cys Gln Gly  
 35 40 45  
 Met Tyr Glu Thr Met Glu Gln Leu Arg Asn Leu Pro Gln Gln Cys Met  
 50 55 60  
 Gln Glu Asp Phe Leu Val His Glu Val Thr Asn Leu Pro Val Thr Glu  
 65 70 75 80  
 Ala Trp Ile Glu Arg Glu Asn Ala Ala Gln Leu Lys Lys Trp Arg Glu  
 85 90 95  
 Thr Arg Gly Glu Leu Gln Tyr Arg Pro Ser Arg Arg Leu His Gly Ser  
 100 105 110

Arg Ala Ile His Glu Glu Arg Arg Arg Gln Gln Pro Pro Leu Gly Pro  
 115 120 125  
 Ser Ser Ser Leu Leu Ser Leu Pro Ser Leu Lys Ser Arg Gly Ser Arg  
 130 135 140  
 Ala Val Gly Gly Ala Pro Ser Pro Pro Pro Val Arg Arg Ala Ser  
 145 150 155 160  
 Ala Gly Pro Val Pro Gly Ala Val Val Ile Ala Glu Gly Leu His Pro  
 165 170 175  
 Ser Leu Pro Ser Pro Thr Gly Asn Ser Thr Pro Leu Gly Thr Ser Lys  
 180 185 190  
 Glu Ile Arg Arg Gln Glu Lys Glu Arg Gln Lys Gln Glu Lys Asp Arg  
 195 200 205  
 Glu Lys Glu Arg Gln Arg Gln Glu Lys Glu Arg Glu Arg Gln Glu Arg  
 210 215 220  
 Ser Gly Arg Ser Gly Lys Arg Ser Lys Arg Arg Asn Ser Arg Ser Arg  
 225 230 235 240  
 Arg Arg Ser Gly Arg Ser Trp Arg Arg Lys Ala Lys Ala Gly Asn Cys  
 245 250 255  
 Pro Cys Val Glu Gly Gln Met Gly Pro Arg His Pro Met Met Val Gly  
 260 265 270  
 Thr Gly Gln Gln Leu Arg Pro Gly Arg Met Leu Thr Phe Asp Leu Trp  
 275 280 285  
 Leu Asp Leu Asp Gly Met Ala Leu Leu Leu Pro Leu Ile Glu Ser Ser  
 290 295 300  
 Pro Gly Arg Leu Ser Gln Leu Pro Leu Ala Gly Ser Ser Phe Phe  
 305 310 315

<210> 676  
 <211> 94  
 <212> PRT  
 <213> Mouse

<400> 676  
 Met Phe Ser Glu Lys Lys His Phe Leu His Thr Ile Gln Asn Pro Glu  
 1 5 10 15  
 Ser Glu Lys Glu Arg Arg Arg Arg Arg Arg Arg Arg Ser Arg Arg  
 20 25 30  
 Arg Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys  
 35 40 45  
 Gln Ala Ser Leu Pro Ser Val Lys Arg Glu Arg Ala Trp His Gly Glu  
 50 55 60  
 Gln Thr Gln Gly Ser Leu Ser Thr Val Arg Gln Glu Ser Ser Pro Gly  
 65 70 75 80  
 His Arg Ala Lys Val Ile Ala Asp Leu Gly Lys Asn Asp Gln  
 85 90

<210> 677  
 <211> 137  
 <212> PRT  
 <213> Mouse

<400> 677  
 Val Arg Trp Lys Met Arg Arg Ser Leu Arg Ala Gly Arg Arg Arg Gln  
 1 5 10 15  
 Thr Ala Gly Arg Lys Ser Lys Ser Pro Pro Lys Val Pro Ile Val Ile  
 20 25 30  
 Gln Asp Asp Ser Leu Pro Thr Gly Pro Pro Pro Gln Ile Arg Ile Leu

```

          35          40          45
Lys Arg Pro Thr Ser Asn Gly Val Val Ser Ser Pro Asn Ser Thr Ser
 50          55          60
Arg Pro Ala Leu Pro Val Lys Ser Leu Ala Gln Arg Glu Ala Glu Tyr
 65          70          75          80
Ala Glu Ala Arg Arg Arg Ile Leu Gly Ser Ala Ser Pro Glu Glu Glu
          85          90          95
Gln Glu Lys Pro Ile Leu Asp Arg Pro Thr Arg Ile Ser Gln Pro Glu
          100          105          110
Asp Ser Arg Gln Pro Ser Asn Val Ile Arg Gln Pro Leu Gly Pro Asp
          115          120          125
Gly Ser Gln Gly Phe Lys Gln Arg Arg
          130          135

```

<210> 678  
 <211> 380  
 <212> PRT  
 <213> Mouse

```

<400> 678
Glu Thr Thr Ile Thr Thr Asp Ser Arg Asp Tyr Gln Met Ala Lys Gly
 1          5          10          15
Lys Arg Lys Asn Leu Thr Asn Arg Asn Gln Asp His Ser Leu Ser Ser
          20          25          30
Glu Pro Ser Thr Pro Thr Ser Ala Ser Pro Gly Tyr Pro Asp Thr Pro
          35          40          45
Glu Lys Gln Asp Ser Asn Leu Lys Ser Tyr Leu Met Met Leu Val Glu
          50          55          60
Asp Ile Lys Lys Gly Phe Asn Asn Ser Leu Lys Glu Val Lys Glu Asn
 65          70          75          80
Thr Ala Lys Glu Val Glu Val Leu Lys Glu Ile Gln Glu Asn Thr Thr
          85          90          95
Lys Gln Val Met Glu Leu Asn Lys Ile Ile Gln Asp Leu Lys Arg Glu
          100          105          110
Val Glu Thr Lys Lys Thr Gln Asn Glu Thr Thr Leu Glu Ile Glu Thr
          115          120          125
Leu Val Lys Lys Ser Gly Thr Ile Asp Val Ser Ile Ser Asn Arg Ile
          130          135          140
Gln Glu Met Glu Glu Arg Ile Ser Gly Ala Glu Asp Ser Ile Glu Asn
 145          150          155          160
Ile Gly Thr Thr Thr Lys Glu Asn Ala Lys Arg Lys Lys Ile Leu Thr
          165          170          175
Gln Asn Ile Gln Lys Ile Gln Asp Lys Met Arg Arg Pro Asn Leu Trp
          180          185          190
Ile Ile Gly Val Asp Glu Asn Glu Asp Ser Gln Leu Lys Gly Pro Ala
          195          200          205
Asn Ile Phe Asn Lys Phe Ile Glu Glu Asn Phe Pro Asn Leu Lys Lys
          210          215          220
Glu Met Ser Met Asn Arg Gln Glu Ala Tyr Arg Thr Pro Asn Arg Leu
 225          230          235          240
Asp Gln Lys Arg Asn Ser Ser Leu His Ile Ile Ile Arg Thr Thr Asn
          245          250          255
Ala Leu Asn Lys Asp Arg Ile Leu Lys Ala Val Arg Glu Lys Ser Gln
          260          265          270
Val Thr Tyr Lys Gly Arg Pro Ile Arg Ile Thr Pro Asp Phe Ser Pro
          275          280          285
Glu Thr Met Lys Ala Arg Arg Ser Trp Thr Asp Val Met Gln Thr Leu

```

```

      290      295      300
Arg Glu His Lys Cys Gln Pro Arg Leu Leu Tyr Pro Ala Lys Leu Ser
305      310      315      320
Ile Thr Ile Asp Gly Glu Thr Lys Val Phe His Asp Lys Thr Lys Phe
      325      330      335
Thr Gln Tyr Leu Ser Met Asn Pro Gly Leu Gln Arg Ile Ile Lys Gly
      340      345      350
Lys His Gln His Lys Asp Gly Asn Tyr Thr Leu Glu Lys Ala Arg Lys
      355      360      365
Arg Ser Phe Asn Lys Pro Lys Arg Arg Gln Pro Lys
      370      375      380

```

<210> 679  
 <211> 210  
 <212> PRT  
 <213> Mouse

```

<400> 679
Tyr Gly Thr His Asn His Cys Trp Leu Ser Leu His Arg Gly Phe Ile
  1      5      10      15
Trp Ser Phe Leu Gly Pro Ala Ala Ala Ile Ile Leu Ile Asn Leu Val
      20      25      30
Phe Tyr Phe Leu Ile Ile Trp Ile Leu Arg Ser Lys Leu Ser Ser Leu
      35      40      45
Asn Lys Glu Val Ser Thr Leu Gln Asp Thr Lys Val Met Thr Phe Lys
      50      55      60
Ala Ile Val Gln Leu Phe Val Leu Gly Cys Ser Trp Gly Ile Gly Leu
      65      70      75      80
Phe Ile Phe Ile Glu Val Gly Lys Thr Val Arg Leu Ile Val Ala Tyr
      85      90      95
Leu Phe Thr Ile Ile Asn Val Leu Gln Gly Val Leu Ile Phe Met Val
      100      105      110
His Cys Leu Leu Asn Arg Gln Val Arg Met Glu Tyr Lys Lys Trp Phe
      115      120      125
His Arg Leu Arg Lys Glu Val Glu Ser Glu Ser Thr Glu Val Ser His
      130      135      140
Ser Thr Thr His Thr Lys Met Gly Leu Ser Leu Asn Leu Glu Asn Phe
      145      150      155      160
Cys Pro Thr Gly Asn Leu His Asp Pro Ser Asp Ser Ile Leu Pro Ser
      165      170      175
Thr Glu Val Ala Gly Val Tyr Leu Ser Thr Pro Arg Ser His Met Gly
      180      185      190
Ala Glu Asp Val Asn Ser Gly Thr His Ala Tyr Trp Ser Arg Thr Ile
      195      200      205
Ser Asp
      210

```

<210> 680  
 <211> 373  
 <212> PRT  
 <213> Mouse

```

<400> 680
Met Lys Glu Tyr Val Met Leu Leu Leu Leu Ala Val Cys Ser Ala Lys
  1      5      10      15
Pro Phe Phe Ser Pro Ser His Thr Ala Leu Lys Asn Met Met Leu Lys
      20      25      30

```



Asp Met Glu Asp Thr Asp Asp Asp Asp Asn Asp Asp Asp Asp Asn Ser  
 35 40 45  
 Leu Phe Pro Thr Lys Glu Pro Val Asn Pro Phe Phe Pro Phe Asp Leu  
 50 55 60  
 Phe Pro Thr Cys Pro Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His  
 65 70 75 80  
 Cys Ser Asp Leu Gly Leu Thr Ser Val Pro Asn Asn Ile Pro Phe Asp  
 85 90 95  
 Thr Arg Met Val Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu  
 100 105 110  
 Asn Asp Phe Lys Gly Leu Thr Ser Leu Tyr Ala Leu Ile Leu Asn Asn  
 115 120 125  
 Asn Lys Leu Thr Lys Ile His Pro Lys Thr Phe Leu Thr Thr Lys Lys  
 130 135 140  
 Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro Leu  
 145 150 155 160  
 Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Asp Asn Lys Val  
 165 170 175  
 Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala Leu His Val  
 180 185 190  
 Leu Glu Met Ser Ala Asn Pro Leu Glu Asn Asn Gly Ile Glu Pro Gly  
 195 200 205  
 Ala Phe Glu Gly Val Thr Val Phe His Ile Arg Ile Ala Glu Ala Lys  
 210 215 220  
 Leu Thr Ser Ile Pro Lys Gly Leu Pro Pro Thr Leu Leu Glu Leu His  
 225 230 235 240  
 Leu Asp Phe Asn Lys Ile Ser Thr Val Glu Leu Glu Asp Leu Lys Arg  
 245 250 255  
 Tyr Arg Glu Leu Gln Arg Leu Gly Leu Gly Asn Asn Arg Ile Thr Asp  
 260 265 270  
 Ile Glu Asn Gly Thr Phe Ala Asn Ile Pro Arg Val Arg Glu Ile His  
 275 280 285  
 Leu Glu His Asn Lys Leu Lys Lys Ile Pro Ser Gly Leu Gln Glu Leu  
 290 295 300  
 Lys Tyr Leu Gln Ile Ile Phe Leu His Tyr Asn Ser Ile Ala Lys Val  
 305 310 315 320  
 Gly Val Asn Asp Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu  
 325 330 335  
 Tyr Ser Ala Ile Ser Leu Phe Asn Asn Pro Met Lys Tyr Trp Glu Ile  
 340 345 350  
 Gln Pro Ala Thr Phe Arg Cys Val Leu Gly Arg Met Ser Val Gln Leu  
 355 360 365  
 Gly Asn Val Gly Lys  
 370

<210> 681  
 <211> 466  
 <212> PRT  
 <213> Mouse

<400> 681  
 Met Trp Gly Cys Trp Leu Gly Leu Leu Leu Leu Leu Ala Gly Gln  
 1 5 10 15  
 Ala Ala Leu Glu Ala Arg Arg Ser Arg Trp Arg Arg Glu Leu Ala Pro  
 20 25 30  
 Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys Gln  
 35 40 45

Glu Gln Asp Met Cys Cys Arg Gly Arg Ala Asp Glu Cys Ala Leu Pro  
 50 55 60  
 Tyr Leu Gly Ala Thr Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr Val  
 65 70 75 80  
 Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Ile Pro Pro  
 85 90 95  
 Pro Phe Pro Pro Val Gln Gly Cys Met His Gly Gly Arg Ile Tyr Pro  
 100 105 110  
 Val Phe Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys His Glu  
 115 120 125  
 Gly Gly His Trp Glu Cys Asp Gln Glu Pro Cys Leu Val Asp Pro Asp  
 130 135 140  
 Met Ile Lys Ala Ile Asn Arg Gly Asn Tyr Gly Trp Gln Ala Gly Asn  
 145 150 155 160  
 His Ser Ala Phe Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr Arg  
 165 170 175  
 Leu Gly Thr Ile Arg Pro Ser Ser Thr Val Met Asn Met Asn Glu Ile  
 180 185 190  
 Tyr Thr Val Leu Gly Gln Gly Glu Val Leu Pro Thr Ala Phe Glu Ala  
 195 200 205  
 Ser Glu Lys Trp Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly Asn  
 210 215 220  
 Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp Arg  
 225 230 235 240  
 Val Ser Ile His Ser Leu Gly His Met Thr Pro Ile Leu Ser Pro Gln  
 245 250 255  
 Asn Leu Leu Ser Cys Asp Thr His His Gln Gln Gly Cys Arg Gly Gly  
 260 265 270  
 Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val Ser  
 275 280 285  
 Asp Asn Cys Tyr Pro Phe Ser Gly Arg Glu Gln Asn Glu Ala Ser Pro  
 290 295 300  
 Thr Pro Arg Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys Arg  
 305 310 315 320  
 Gln Ala Thr Ser Arg Cys Pro Asn Gly Gln Val Asp Ser Asn Asp Ile  
 325 330 335  
 Tyr Gln Val Thr Pro Ala Tyr Arg Leu Gly Ser Asp Glu Lys Glu Ile  
 340 345 350  
 Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu Val  
 355 360 365  
 His Glu Asp Phe Phe Leu Tyr Gln Arg Gly Ile Tyr Ser His Thr Pro  
 370 375 380  
 Val Ser Gln Gly Arg Pro Glu Gln Tyr Arg Arg His Gly Thr His Ser  
 385 390 395 400  
 Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg Thr  
 405 410 415  
 Ile Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Trp Trp Gly Glu  
 420 425 430  
 Arg Gly His Phe Arg Ile Val Arg Gly Thr Asn Glu Cys Asp Ile Glu  
 435 440 445  
 Thr Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met Gly  
 450 455 460  
 His His  
 465

&lt;210&gt; 682

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 682

```

Met Arg Leu Arg Leu Leu Ala Leu Ala Ala Val Leu Leu Gly Pro
 1      5      10      15
Ala Pro Glu Val Cys Gly Ala Leu Asn Val Thr Val Ser Pro Gly Pro
      20      25      30
Val Val Asp Tyr Leu Glu Gly Glu Asn Ala Thr Leu Leu Cys His Val
      35      40      45
Ser Gln Lys Arg Arg Lys Asp Ser Leu Leu Ala Val Arg Trp Phe Phe
      50      55      60
Ala Pro Asp Gly Ser Gln Glu Ala Leu Met Val Lys Met Thr Lys Leu
      65      70      75      80
Arg Ile Ile Gln Tyr Tyr Gly Asn Phe Ser Arg Thr Ala Asn Gln Gln
      85      90      95
Arg Leu Arg Leu Leu Glu Glu Arg Arg Gly Val Leu Tyr Arg Leu Ser
      100      105      110
Val Leu Thr Leu Arg Pro Thr Asp Gln Gly Gln Tyr Val Cys Lys Val
      115      120      125
Gln Glu Ile Ser Lys His Arg Asn Lys Trp Thr Ala Trp Ser Asn Gly
      130      135      140
Ser Ser Ala Thr Glu Met Arg Val Ile Ser Leu Lys Ala Gly Glu Asp
      145      150      155      160
Ser Ser Phe Glu Lys Lys Lys Val Thr Trp Ala Phe Phe Glu Asp Leu
      165      170      175
Tyr Val Tyr Ala Val Leu Val Cys Cys Val Gly Ile Leu Ser Val Leu
      180      185      190
Leu Phe Thr Leu Val Ile Ala Cys Ser Leu Cys Phe Thr Arg Gly Asn
      195      200      205
Gln Glu
      210

```

&lt;210&gt; 683

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 683

```

Met Asp Phe Trp Leu Trp Leu Leu Tyr Phe Leu Pro Val Ser Gly Ala
 1      5      10      15
Leu Arg Val Leu Pro Glu Val Gln Leu Asn Val Glu Trp Gly Gly Ser
      20      25      30
Ile Ile Ile Glu Cys Pro Leu Pro Gln Leu His Val Arg Met Tyr Leu
      35      40      45
Cys Arg Gln Met Ala Lys Pro Gly Ile Cys Ser Thr Val Val Ser Asn
      50      55      60
Thr Phe Val Lys Lys Glu Tyr Glu Arg Arg Val Thr Leu Thr Pro Cys
      65      70      75      80
Leu Asp Lys Lys Leu Phe Leu Val Glu Met Thr Gln Leu Thr Glu Asn
      85      90      95
Asp Asp Gly Ile Tyr Ala Cys Gly Val Gly Met Lys Thr Asp Lys Gly
      100      105      110
Lys Thr Gln Lys Ile Thr Leu Asn Val His Asn Glu Tyr Pro Glu Pro
      115      120      125
Phe Trp Glu Asp Glu Trp Thr Ser Glu Arg Pro Arg Trp Leu His Arg
      130      135      140

```

```

Phe Leu Gln His Gln Met Pro Trp Leu His Gly Ser Glu His Pro Ser
145          150          155          160
Ser Ser Gly Val Ile Ala Lys Val Thr Thr Pro Ala Ser Lys Thr Glu
          165          170          175
Ala Pro Pro Val His Gln Pro Ser Ser Ile Thr Ser Val Thr Gln His
          180          185          190
Pro Arg Val Tyr Arg Ala Phe Ser Val Ser Ala Thr Lys Ser Pro Ala
          195          200          205
Leu Leu Pro Ala Thr Thr Ala Ser Lys Thr Ser Thr Gln Gln Ala Ile
          210          215          220
Arg Pro Leu Glu Ala Ser Tyr Ser His His Thr Arg Leu His Glu Gln
225          230          235          240
Arg Thr Arg His His Gly Pro His Tyr Gly Arg Glu Asp Arg Gly
          245          250          255

```

```

<210> 684
<211> 228
<212> PRT
<213> Mouse

```

```

<400> 684
Met Lys Ala Leu Arg Ala Val Leu Leu Ile Leu Leu Leu Ser Gly Gln
1          5          10          15
Pro Gly Ser Gly Trp Ala Gln Glu Asp Gly Asp Ala Asp Pro Glu Pro
          20          25          30
Glu Asn Tyr Asn Tyr Asp Asp Asp Asp Glu Glu Glu Glu Glu Glu
          35          40          45
Thr Asn Met Ile Pro Gly Ser Arg Asp Arg Ala Pro Leu Gln Cys Tyr
          50          55          60
Phe Cys Gln Val Leu His Ser Gly Glu Ser Cys Asn Gln Thr Gln Ser
65          70          75          80
Cys Ser Ser Ser Lys Pro Phe Cys Ile Thr Leu Val Ser His Ser Gly
          85          90          95
Thr Asp Lys Gly Tyr Leu Thr Thr Tyr Ser Met Trp Cys Thr Asp Thr
          100          105          110
Cys Gln Pro Ile Ile Lys Thr Val Gly Gly Thr Gln Met Thr Gln Thr
          115          120          125
Cys Cys Gln Ser Thr Leu Cys Asn Ile Pro Pro Trp Gln Asn Pro Gln
          130          135          140
Val Gln Asn Pro Leu Gly Gly Arg Ala Asp Ser Pro Leu Glu Ser Gly
145          150          155          160
Thr Arg His Pro Gln Gly Gly Lys Phe Ser His Pro Gln Val Val Lys
          165          170          175
Ala Ala His Pro Gln Ser Asp Gly Ala Asn Leu Pro Lys Ser Gly Lys
          180          185          190
Ala Asn Gln Pro Gln Gly Ser Gly Ala Gly Tyr Pro Ser Gly Trp Thr
          195          200          205
Lys Phe Gly Asn Ile Ala Leu Leu Ser Phe Phe Thr Cys Leu Trp
          210          215          220
Ala Ser Gly Ala
225

```

```

<210> 685
<211> 242
<212> PRT
<213> Mouse

```

&lt;400&gt; 685

```

Met Ala Ser Gly Trp Phe Tyr Leu Ser Cys Met Val Leu Gly Ser Leu
 1      5      10      15
Gly Ser Met Cys Ile Leu Phe Thr Ala Tyr Trp Met Gln Tyr Trp Arg
 20      25      30
Gly Gly Phe Ala Trp Asp Gly Thr Val Leu Met Phe Asn Trp His Pro
 35      40      45
Val Leu Met Val Ala Gly Met Val Val Leu Tyr Gly Ala Ala Ser Leu
 50      55      60
Val Tyr Arg Leu Pro Ser Ser Trp Val Gly Pro Arg Leu Pro Trp Lys
 65      70      75      80
Val Leu His Ala Ala Leu His Leu Leu Ala Phe Thr Cys Thr Val Val
 85      90      95
Gly Leu Ile Ala Val Phe Arg Phe His Asn His Ser Arg Ile Ala His
100      105      110
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Val Leu Phe
115      120      125
Ala Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
130      135      140
Ser Gln Trp Leu Arg Ser Leu Leu Lys Pro Leu His Val Phe Phe Gly
145      150      155      160
Ala Cys Ile Leu Ser Leu Ser Ile Thr Ser Val Ile Ser Gly Ile Asn
165      170      175
Glu Lys Leu Phe Phe Val Leu Lys Asn Ala Thr Lys Pro Tyr Ser Ser
180      185      190
Leu Pro Gly Glu Ala Val Phe Ala Asn Ser Thr Gly Leu Leu Val Val
195      200      205
Ala Phe Gly Leu Leu Val Leu Tyr Val Leu Leu Ala Ser Ser Trp Lys
210      215      220
Arg Pro Asp Pro Gly Ala Leu Thr Asp Arg Gln Pro Leu Leu His Asp
225      230      235      240
Arg Glu

```

&lt;210&gt; 686

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 686

```

Met Arg Leu Pro Leu Pro Leu Leu Leu Phe Gly Cys Arg Ala Ile
 1      5      10      15
Leu Gly Ser Ala Gly Asp Arg Val Ser Leu Ser Ala Ser Ala Pro Thr
 20      25      30
Leu Asp Asp Glu Glu Lys Tyr Ser Ala His Met Pro Ala His Leu Arg
 35      40      45
Cys Asp Ala Cys Arg Ala Val Ala Phe Gln Met Gly Gln Arg Leu Ala
 50      55      60
Lys Ala Glu Ala Lys Ser His Thr Pro Asp Ala Ser Gly Leu Gln Glu
 65      70      75      80
Leu Ser Glu Ser Thr Tyr Thr Asp Val Leu Asp Gln Thr Cys Ser Gln
 85      90      95
Asn Trp Gln Ser Tyr Gly Val His Glu Val Asn Gln Met Lys Arg Leu
100      105      110
Thr Gly Pro Gly Leu Ser Lys Gly Pro Glu Pro Arg Ile Ser Val Met
115      120      125
Ile Ser Gly Gly Pro Trp Pro Asn Arg Leu Ser Lys Thr Cys Phe His

```

```

      130              135              140
Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala Tyr Arg Gln
145              150              155              160
Gly Gln Ala Asn Leu Glu Ala Leu Leu Cys Gly Gly Thr His Gly Pro
      165              170              175
Cys Ser Gln Glu Ile Leu Ala Gln Arg Glu Glu Leu
      180              185

```

<210> 687  
 <211> 247  
 <212> PRT  
 <213> Mouse

```

<400> 687
Met Ile Pro Gln Val Val Thr Ser Glu Thr Val Thr Val Ile Ser Pro
 1              5              10              15
Asn Gly Ile Ser Phe Pro Gln Thr Asp Lys Pro Gln Pro Ser His Gln
 20              25              30
Ser Gln Asp Arg Leu Lys Lys His Leu Lys Ala Glu Ile Lys Val Met
 35              40              45
Ala Ala Ile Gln Ile Met Cys Ala Val Met Val Leu Ser Leu Gly Ile
 50              55              60
Ile Leu Ala Ser Val Pro Ser Asn Leu His Phe Thr Ser Val Phe Ser
 65              70              75              80
Ile Leu Leu Glu Ser Gly Tyr Pro Phe Val Gly Ala Leu Phe Phe Ala
      85              90              95
Ile Ser Gly Ile Leu Ser Ile Val Thr Glu Lys Lys Met Thr Lys Pro
      100              105              110
Leu Val His Ser Ser Leu Ala Leu Ser Ile Leu Ser Val Leu Ser Ala
      115              120              125
Leu Thr Gly Ile Ala Ile Leu Ser Val Ser Leu Ala Ala Leu Glu Pro
      130              135              140
Ala Leu Gln Gln Cys Lys Leu Ala Phe Thr Gln Leu Asp Thr Thr Gln
145              150              155              160
Asp Ala Tyr His Phe Phe Ser Pro Glu Pro Leu Asn Ser Cys Phe Val
      165              170              175
Ala Lys Ala Ala Leu Thr Gly Val Phe Ser Leu Met Leu Ile Ser Ser
      180              185              190
Val Leu Glu Leu Gly Leu Ala Val Leu Thr Ala Thr Leu Trp Trp Lys
      195              200              205
Gln Ser Ser Ser Ala Phe Ser Gly Asn Val Ile Phe Leu Ser Gln Asn
210              215              220
Ser Lys Asn Lys Ser Ser Val Ser Ser Glu Ser Leu Cys Asn Pro Thr
225              230              235              240
Tyr Glu Asn Ile Leu Thr Ser
      245

```

<210> 688  
 <211> 121  
 <212> PRT  
 <213> Mouse

```

<400> 688
Tyr Gln Arg Arg Ser Lys Thr Leu Glu Glu Leu Ala Asn Asp Ile Lys
 1              5              10              15
Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Thr Lys Gly Ser Asp
      20              25              30

```

```

Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala
    35      40      45
Leu Arg Pro Pro Lys Ala Ala Pro Pro Arg Pro Gly Thr Phe Thr Pro
    50      55      60
Thr Pro Ser Val Ser Ser Gln Ala Leu Ser Ser Pro Arg Leu Pro Arg
    65      70      75      80
Val Asp Glu Pro Pro Pro Gln Ala Val Ser Leu Thr Pro Gly Gly Val
    85      90      95
Ser Ser Ser Ala Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro
    100     105     110
Ala Gln Ser Gln Ala Gly Ser Leu Val
    115     120

```

<210> 689  
 <211> 255  
 <212> PRT  
 <213> Mouse

```

<400> 689
Pro Ala Phe Ser Ser Ala Ala Met Ser Trp Ser Pro Ile Leu Pro Phe
    1      5      10      15
Leu Ser Leu Leu Leu Leu Phe Pro Leu Glu Val Pro Arg Ala Ala
    20      25      30
Thr Ala Ser Leu Ser Gln Ala Ser Ser Glu Gly Thr Thr Thr Cys Lys
    35      40      45
Val His Asp Val Cys Leu Leu Gly Pro Arg Pro Leu Pro Pro Ser Pro
    50      55      60
Pro Val Arg Val Ser Leu Tyr Tyr Glu Ser Leu Cys Gly Ala Cys Arg
    65      70      75      80
Tyr Phe Leu Val Arg Asp Leu Phe Pro Thr Trp Leu Met Val Met Glu
    85      90      95
Ile Met Asn Ile Thr Leu Val Pro Tyr Gly Asn Ala Gln Glu Arg Asn
    100     105     110
Val Ser Gly Thr Trp Glu Phe Thr Cys Gln His Gly Glu Leu Glu Cys
    115     120     125
Arg Leu Asn Met Val Glu Ala Cys Leu Leu Asp Lys Leu Glu Lys Glu
    130     135     140
Ala Ala Phe Leu Thr Ile Val Cys Met Glu Glu Met Asp Asp Met Glu
    145     150     155     160
Lys Lys Leu Gly Pro Cys Leu Gln Val Tyr Ala Pro Glu Val Ser Pro
    165     170     175
Glu Ser Ile Met Glu Cys Ala Thr Gly Lys Arg Gly Thr Gln Leu Met
    180     185     190
His Glu Asn Ala Gln Leu Thr Asp Ala Leu His Pro Pro His Glu Tyr
    195     200     205
Val Pro Trp Val Leu Val Asn Glu Lys Pro Leu Lys Asp Pro Ser Glu
    210     215     220
Leu Leu Ser Ile Val Cys Gln Leu Asp Gln Gly Thr Glu Lys Pro Asp
    225     230     235     240
Ile Cys Ser Ser Ile Ala Asp Ser Pro Arg Lys Val Cys Tyr Lys
    245     250     255

```

<210> 690  
 <211> 255  
 <212> PRT  
 <213> Mouse

&lt;400&gt; 690

```

Met Val Trp Thr Gln Asp Arg Leu His Asp Arg Gln Arg Val Val His
 1          5          10          15
Trp Asp Leu Ser Gly Asp Pro Gly Ser Gln Arg Arg Arg Leu Val Asp
          20          25          30
Met Tyr Ser Ala Gly Glu Gln Arg Val Tyr Glu Pro Arg Asp Arg Asp
          35          40          45
Arg Leu Leu Leu Ser Pro Ser Ala Phe His Asp Gly Asn Phe Ser Leu
          50          55          60
Leu Ile Arg Ala Val Glu Arg Gly Asp Glu Gly Val Tyr Thr Cys Asn
          65          70          75          80
Leu His His His Tyr Cys His Leu Asp Glu Ser Leu Ala Val Arg Leu
          85          90          95
Glu Val Thr Asp Asp Pro Leu Leu Ser Arg Ala Tyr Trp Asp Gly Glu
          100          105          110
Lys Glu Val Leu Val Val Ala His Gly Ala Pro Ala Leu Met Thr Cys
          115          120          125
Ile Asn Arg Ala His Val Trp Thr Asp Arg His Leu Glu Glu Ala Gln
          130          135          140
Gln Val Val His Trp Asp Arg Gln Leu Pro Gly Val Ser His Asp Arg
          145          150          155          160
Ala Asp Arg Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr
          165          170          175          180
Gly Pro Pro Phe Leu Arg Asp Arg Val Ser Val Asn Thr Asn Ala Phe
          180          185          190
Ala Arg Gly Asp Phe Ser Leu Arg Ile Asp Glu Leu Glu Arg Ala Asp
          195          200          205
Glu Gly Ile Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu His
          210          215          220
Glu Arg Arg Val Phe His Leu Gln Val Thr Glu Pro Ala Phe Glu Pro
          225          230          235          240
Pro Ala Arg Ala Ser Pro Gly Asn Gly Ser Gly His Ser Ser Ala
          245          250          255

```

&lt;210&gt; 691

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 691

```

Met Lys Leu Lys Gln Arg Val Val Leu Leu Ala Ile Leu Leu Val Ile
 1          5          10          15
Phe Ile Phe Thr Lys Val Phe Leu Ile Asp Asn Leu Asp Thr Ser Ala
          20          25          30
Ala Asn Arg Glu Asp Gln Arg Ala Phe His Arg Met Met Thr Gly Leu
          35          40          45
Arg Val Glu Leu Val Pro Lys Leu Asp His Thr Leu Gln Ser Pro Trp
          50          55          60
Glu Ile Ala Ala Gln Trp Val Val Pro Arg Glu Val Tyr Pro Glu Glu
          65          70          75          80
Thr Pro Glu Leu Gly Ala Ile Met His Ala Met Ala Thr Lys Lys Ile
          85          90          95
Ile Lys Ala Asp Val Gly Tyr Lys Gly Thr Gln Leu Lys Ala Leu Leu
          100          105          110
Ile Leu Glu Gly Gly Gln Lys Val Val Phe Lys Pro Lys Arg Tyr Ser
          115          120          125
Arg Asp Tyr Val Val Glu Gly Glu Pro Tyr Ala Gly Tyr Asp Arg His
          130          135          140

```



130						135						140					
Asn	Ala	Glu	Val	Ala	Ala	Phe	His	Leu	Asp	Arg	Ile	Leu	Gly	Phe	Arg		
145					150					155					160		
Arg	Ala	Pro	Leu	Val	Val	Gly	Arg	Tyr	Val	Asn	Leu	Arg	Thr	Glu	Val		
				165					170					175			
Lys	Pro	Val	Ala	Thr	Glu	Gln	Leu	Leu	Ser	Thr	Phe	Leu	Thr	Val	Gly		
			180					185					190				
Asn	Asn	Thr	Cys	Phe	Tyr	Gly	Lys	Cys	Tyr	Tyr	Cys	Arg	Glu	Thr	Glu		
		195					200					205					
Pro	Ala	Cys	Ala	Asp	Gly	Asp	Met	Met	Glu	Gly	Ser	Val	Thr	Leu	Trp		
		210			215							220					
Leu	Pro	Asp	Val	Trp	Pro	Leu	Gln	Lys	His	Arg	His	Pro	Trp	Gly	Arg		
225					230					235					240		
Thr	Tyr	Arg	Glu	Gly	Lys	Leu	Ala	Arg	Trp	Glu	Tyr	Asp	Glu	Ser			
			245						250					255			

<210> 692  
 <211> 255  
 <212> PRT  
 <213> Mouse

<400> 692																	
Met	Gln	Thr	Met	Trp	Gly	Ser	Gly	Glu	Leu	Leu	Val	Ala	Trp	Phe	Leu		
1				5				10						15			
Val	Leu	Ala	Ala	Asp	Gly	Thr	Thr	Glu	His	Val	Tyr	Arg	Pro	Ser	Arg		
			20					25					30				
Arg	Val	Cys	Thr	Val	Gly	Ile	Ser	Gly	Gly	Ser	Ile	Ser	Glu	Thr	Phe		
		35				40					45						
Val	Gln	Arg	Val	Tyr	Gln	Pro	Tyr	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg		
	50				55						60						
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser		
65				70					75					80			
Pro	Gly	Val	Thr	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	Gly	Trp		
				85				90						95			
Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln		
			100					105					110				
Pro	Pro	Cys	Gly	Asn	Gly	Gly	Ser	Cys	Ile	Arg	Pro	Gly	His	Cys	Arg		
		115					120					125					
Cys	Pro	Val	Gly	Trp	Gln	Gly	Asp	Thr	Cys	Gln	Thr	Asp	Val	Asp	Glu		
		130				135						140					
Cys	Ser	Thr	Gly	Glu	Ala	Ser	Cys	Pro	Gln	Arg	Cys	Val	Asn	Thr	Val		
145				150					155					160			
Gly	Ser	Tyr	Trp	Cys	Gln	Gly	Trp	Glu	Gly	Gln	Ser	Pro	Ser	Ala	Asp		
			165					170						175			
Gly	Thr	Arg	Cys	Leu	Ser	Lys	Glu	Gly	Pro	Ser	Pro	Val	Ala	Pro	Asn		
			180				185					190					
Pro	Thr	Ala	Gly	Val	Asp	Ser	Met	Ala	Arg	Glu	Glu	Val	Tyr	Arg	Leu		
		195				200						205					
Gln	Ala	Arg	Val	Asp	Val	Leu	Glu	Gln	Lys	Leu	Gln	Leu	Val	Leu	Ala		
	210				215						220						
Pro	Leu	His	Ser	Leu	Ala	Ser	Arg	Ser	Thr	Glu	His	Gly	Leu	Gln	Asp		
225				230					235					240			
Pro	Gly	Ser	Leu	Leu	Ala	His	Ser	Phe	Gln	Gln	Leu	Asp	Arg	Ile			
			245						250					255			

<210> 693  
 <211> 255

<212> PRT  
<213> Mouse

<400> 693

```

Met Arg Leu Thr Val Gly Ala Leu Leu Ala Cys Ala Ala Leu Gly Leu
 1          5          10          15
Cys Leu Ala Val Pro Asp Lys Thr Val Lys Trp Cys Ala Val Ser Glu
          20          25          30
His Glu Asn Thr Lys Cys Ile Ser Phe Arg Asp His Met Lys Thr Val
          35          40          45
Leu Pro Pro Asp Gly Pro Arg Leu Ala Cys Val Lys Lys Thr Ser Tyr
          50          55          60
Pro Asp Cys Ile Lys Ala Ile Ser Ala Ser Glu Ala Asp Ala Met Thr
          65          70          75          80
Leu Asp Gly Gly Trp Val Tyr Asp Ala Gly Leu Thr Pro Asn Asn Leu
          85          90          95
Lys Pro Val Ala Ala Glu Phe Tyr Gly Ser Val Glu His Pro Gln Thr
          100          105          110
Tyr Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Thr Asp Phe Gln Leu
          115          120          125
Asn Gln Leu Glu Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
          130          135          140
Ala Gly Trp Val Ile Pro Ile Gly Leu Leu Phe Cys Lys Leu Ser Glu
          145          150          155          160
Pro Arg Ser Pro Leu Glu Lys Ala Val Ser Ser Phe Phe Ser Gly Ser
          165          170          175
Cys Val Pro Cys Ala Asp Pro Val Ala Phe Pro Lys Leu Cys Gln Leu
          180          185          190
Cys Pro Gly Cys Gly Cys Ser Ser Thr Gln Pro Phe Phe Gly Tyr Val
          195          200          205
Gly Ala Phe Lys Cys Leu Lys Asp Gly Gly Gly Asp Val Ala Phe Val
          210          215          220
Lys His Thr Thr Ile Phe Glu Val Leu Pro Glu Lys Ala Asp Arg Asp
          225          230          235          240
Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp
          245          250          255

```

<210> 694  
<211> 255  
<212> PRT  
<213> Mouse

<400> 694

```

Gly Ala Pro Thr Pro Ala Tyr Val Arg Ser Ala Arg Arg Thr Glu Pro
 1          5          10          15
Leu Ala Ser Gly Ala Arg Ser Arg Leu Cys Gln Cys Arg Arg Val Pro
          20          25          30
Ala Arg Lys Gln Gly Pro Gln Glu Gln Gly Gly Ser Gly Glu Ser Thr
          35          40          45
Thr Ser Ser Pro Gln Trp Trp Arg Arg Trp Arg Arg Leu Trp Ser Thr
          50          55          60
Cys Ser Cys Ser Ala Asp Arg His Thr Gly Ser His Thr Asp Leu
          65          70          75          80
Lys Glu Glu Thr Pro Ser Trp Thr Gln Ile Ser Val Val Phe Arg Lys
          85          90          95
Asp Gly Gln Asp Glu Leu Gln Ala Ala His Lys Ala His Gly Ser Gly
          100          105          110

```

```

Ser Pro Leu Thr Asn Gln Glu Ile Pro Ser Ser Ser Gly Ser Gly Phe
      115      120      125
Ile Val Ser Glu Asp Gly Leu Ile Val Thr Asn Ala His Val Leu Thr
      130      135      140
Asn Gln Gln Lys Ile Gln Val Glu Leu Gln Ser Gly Ala Arg Tyr Glu
      145      150      155      160
Ala Thr Val Lys Asp Ile Asp His Lys Leu Asp Leu Ala Leu Ile Lys
      165      170      175
Ile Glu Pro Asp Thr Glu Leu Pro Val Leu Leu Leu Gly Arg Ser Ser
      180      185      190
Asp Leu Arg Ala Gly Glu Phe Val Val Ala Leu Gly Ser Pro Phe Ser
      195      200      205
Leu Gln Asn Thr Val Thr Ala Gly Ile Val Ser Thr Thr Gln Arg Gly
      210      215      220
Gly Arg Glu Leu Gly Leu Lys Asn Ser Asp Ile Asp Tyr Ile Gln Thr
      225      230      235      240
Asp Ala Ile Ile Asn His Gly Asn Ser Gly Gly Pro Leu Val Asn
      245      250      255

```

<210> 695  
 <211> 174  
 <212> PRT  
 <213> Mouse

```

<400> 695
Met Pro Ala Cys Arg Leu Cys Leu Leu Ala Ala Gly Leu Leu Leu Gly
  1      5      10      15
Leu Leu Leu Phe Thr Pro Ile Ser Ala Thr Gly Thr Asp Ala Glu Lys
      20      25      30
Pro Gly Glu Cys Pro Gln Leu Glu Pro Ile Thr Asp Cys Val Leu Glu
      35      40      45
Cys Thr Leu Asp Lys Asp Cys Ala Asp Asn Arg Lys Cys Cys Gln Ala
      50      55      60
Gly Cys Ser Ser Val Cys Ser Lys Pro Asn Gly Gly Pro Ser Glu Gly Glu
      65      70      75      80
Leu Ser Gly Thr Asp Thr Lys Leu Ser Glu Thr Gly Thr Thr Thr Gln
      85      90      95
Ser Ala Gly Leu Asp His Thr Thr Lys Pro Pro Gly Gly Gln Val Ser
      100      105      110
Thr Lys Pro Pro Ala Val Thr Arg Glu Gly Leu Gly Val Arg Glu Lys
      115      120      125
Gln Gly Thr Cys Pro Ser Val Asp Ile Pro Lys Leu Gly Leu Cys Glu
      130      135      140
Asp Gln Cys Gln Val Asp Ser Gln Cys Ser Gly Asn Met Lys Cys Cys
      145      150      155      160
Arg Asn Gly Cys Gly Lys Met Ala Cys Thr Thr Pro Lys Phe
      165      170

```

<210> 696  
 <211> 193  
 <212> PRT  
 <213> Mouse

```

<400> 696
Leu Ala Thr Leu Val Gln Val Ser Arg Ile Arg Ala Tyr Ser Gln Gly
  1      5      10      15
Gln Thr Gln Asp Gln Gln Gly Ser Ser Ser Leu Asp Lys Val Ala Val

```

```

      20      25      30
Pro Arg Glu Gln Thr His Ser Gly Leu Glu Gln Ile Gln Gln Ile Gln
      35      40      45
Gln Gln Leu Thr Gln Phe Asn Ala Ser Leu Ala Gly Leu Cys Arg Pro
      50      55      60
Cys Pro Trp Asp Trp Glu Phe Gln Gly Ser Cys Tyr Leu Phe Ser
      65      70      75      80
Arg Thr Leu Gly Ser Trp Glu Thr Ser Ala Ser Ser Cys Glu Asp Leu
      85      90      95
Gly Ala His Leu Val Ile Val Asn Ser Val Ser Glu Gln Arg Phe Met
      100      105      110
Lys Tyr Trp Asn Val Arg Lys Asn Gln Arg Ser Trp Ile Gly Leu Ser
      115      120      125
Asp His Ile His Glu Gly Ser Trp Gln Trp Val Asp Gly Ser Ala Leu
      130      135      140
Lys Phe Ser Phe Trp Lys Glu Gly Glu Pro Asn Asn Asp Gly Asp Glu
      145      150      155      160
Asp Cys Val Glu Leu Phe Met Asp Asp Trp Asn Asp Asn Lys Cys Thr
      165      170      175
Glu Gln Asn Phe Trp Val Cys Glu Gln Pro Ser Ala Pro Cys Pro His
      180      185      190
His

```

<210> 697  
 <211> 173  
 <212> PRT  
 <213> Mouse

```

<400> 697
Val Arg Asn Gly Asp Leu Phe Phe Lys Lys Val Gln Val Glu Asp Gly
      1      5      10      15
Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
      20      25      30
Ser Val Glu Leu Lys Val Tyr Asn Phe Thr Leu His Gly His His Asp
      35      40      45
Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
      50      55      60
Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
      65      70      75      80
Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
      85      90      95
Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
      100      105      110
Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
      115      120      125
Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
      130      135      140
Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
      145      150      155      160
Ser Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
      165      170

```

<210> 698  
 <211> 88  
 <212> PRT  
 <213> Mouse

&lt;400&gt; 698

```

Met Glu Glu Ile Thr Cys Ala Phe Leu Leu Leu Leu Ala Gly Leu Pro
 1          5          10          15
Ala Leu Glu Ala Ser Asp Pro Val Asp Lys Asp Ser Pro Phe Tyr Tyr
          20          25          30
Asp Trp Glu Ser Leu Gln Leu Gly Gly Leu Ile Phe Gly Gly Leu Leu
          35          40          45
Cys Ile Ala Gly Ile Ala Met Ala Leu Ser Gly Lys Cys Lys Cys Arg
          50          55          60
Arg Thr His Lys Pro Ser Ser Leu Pro Gly Lys Ala Thr Pro Leu Ile
65          70          75          80
Ile Pro Gly Ser Ala Asn Thr Cys
          85

```

&lt;210&gt; 699

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 699

```

Met Tyr Ser Glu Gly Ala Pro Phe Trp Thr Gly Ile Val Ala Met Leu
 1          5          10          15
Ala Gly Ala Val Ala Phe Leu His Lys Lys Arg Gly Gly Thr Cys Trp
          20          25          30
Ala Leu Met Arg Thr Leu Leu Val Leu Ala Ser Phe Cys Thr Ala Val
          35          40          45
Ala Ala Ile Val Ile Gly Ser Arg Glu Leu Asn Tyr Tyr Trp Tyr Phe
          50          55          60
Leu Gly Asp Asp Val Cys Gln Arg Asp Ser Ser Tyr Gly Trp Ser Thr
65          70          75          80
Met Pro Arg Thr Thr Pro Val Pro Glu Glu Ala Asp Arg Ile Ala Leu
          85          90          95
Cys Ile Tyr Tyr Thr Ser Met Leu Lys Thr Leu Leu Met Ser Leu Gln
          100          105          110
Ala Met Leu Leu Gly Ile Trp Val Leu Leu Leu Ala Ser Leu Thr
          115          120          125
Pro Val Cys Val Tyr Ile Trp Lys Arg Phe Phe Thr Lys Ala Glu Thr
          130          135          140
Glu Glu Lys Lys Leu Leu Gly Ala Ala Val Ile
145          150          155

```

&lt;210&gt; 700

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 700

```

Met Leu Gln His Thr Ser Leu Val Leu Leu Leu Ala Ser Ile Trp Thr
 1          5          10          15
Thr Arg His Pro Val Gln Gly Ala Asp Leu Val Gln Asp Leu Ser Ile
          20          25          30
Ser Thr Cys Arg Ile Met Gly Val Ala Leu Val Gly Arg Asn Lys Asn
          35          40          45
Pro Gln Met Asn Phe Thr Glu Ala Asn Glu Ala Cys Lys Met Leu Gly
          50          55          60
Leu Thr Leu Ala Ser Arg Asp Gln Val Glu Ser Ala Gln Lys Ser Gly

```

```

65          70          75          80
Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Glu Gln Phe Ser Val Ile
      85          90          95
Pro Arg Ile Phe Ser Asn Pro Arg Cys Gly Lys Asn Gly Lys Gly Val
      100         105         110
Leu Ile Trp Asn Ala Pro Ser Ser Gln Lys Phe Lys Ala Tyr Cys His
      115         120         125
Asn Ser Ser Asp Thr Trp Val Asn Ser Cys Ile Pro Glu Ile Val Thr
      130         135         140
Thr Phe Tyr Pro Val Leu Asp Thr Gln Thr Pro Ala Thr Glu Phe Ser
145         150         155         160
Val Ser Ser Ser Ala Tyr Leu Ala Ser Ser Pro Asp Ser Thr Thr Pro
      165         170         175
Val Ser Ala Thr Thr Arg Ala Pro Pro Leu Thr Ser Met Ala Arg Lys
      180         185         190
Thr Lys Lys Ile Cys Ile Thr Glu Val Tyr Thr Glu Pro Ile Thr Met
      195         200         205
Ala Thr Glu Thr Glu Ala Phe Val Ala Ser Gly Ala Ala Phe Lys Asn
210         215         220
Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu Leu Val Leu Ala
225         230         235         240
Leu Leu Phe Phe Gly Ala Ala Ala Val Leu Ala Val Cys Tyr Val
      245         250         255

```

```

<210> 701
<211> 91
<212> PRT
<213> Mouse

```

```

<400> 701
Met Val Trp Ala Asn Leu Ala Val Phe Val Ile Cys Phe Leu Pro Leu
 1          5          10          15
His Val Val Leu Thr Val Gln Val Ser Leu Asn Leu Asn Thr Cys Ala
      20          25          30
Ala Arg Asp Thr Phe Ser Arg Ala Leu Ser Ile Thr Gly Lys Leu Ser
      35          40          45
Asp Thr Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Met Ala Arg
      50          55          60
Glu Phe Gln Glu Ala Ser Lys Pro Ala Thr Ser Ser Asn Thr Pro His
65          70          75          80
Lys Ser Gln Asp Ser Gln Ile Leu Ser Leu Thr
      85          90

```

```

<210> 702
<211> 244
<212> PRT
<213> Mouse

```

```

<400> 702
Gly Trp Gln Gly Ala Pro Asp Pro Arg Gly Leu Gly Gln Leu Ser Gln
 1          5          10          15
Pro Tyr Met Gly Gly Glu Met Pro Trp Thr Ile Leu Leu Phe Ala Ser
      20          25          30
Gly Ser Leu Ala Ile Pro Ala Pro Ser Ile Ser Leu Val Pro Pro Tyr
      35          40          45
Pro Ser Ser His Glu Asp Pro Ile Tyr Ile Ser Cys Thr Ala Pro Gly
50          55          60

```

```

Asp Ile Leu Gly Ala Asn Phe Thr Leu Phe Arg Gly Gly Glu Val Val
65      70      -      75
Gln Leu Leu Gln Ala Pro Ser Asp Arg Pro Asp Val Thr Phe Asn Val
      85      90      95
Thr Gly Gly Gly Ser Gly Gly Gly Gly Glu Ala Ala Gly Gly Asn Phe
      100      105      110
Cys Cys Gln Tyr Gly Val Met Gly Glu His Ser Gln Pro Gln Leu Ser
      115      120      125
Asp Phe Ser Gln Gln Val Gln Val Ser Phe Pro Val Pro Thr Trp Ile
      130      135      140
Leu Ala Leu Ser Leu Ser Leu Ala Gly Ala Val Leu Phe Ser Gly Leu
      145      150      155      160
Val Ala Ile Thr Val Leu Val Arg Lys Ala Lys Ala Lys Asn Leu Gln
      165      170      175
Lys Gln Arg Glu Arg Glu Ser Cys Trp Ala Gln Ile Asn Phe Thr Asn
      180      185      190
Thr Asp Met Ser Phe Asp Asn Ser Leu Phe Ala Ile Ser Thr Lys Met
      195      200      205
Thr Gln Glu Asp Ser Val Ala Thr Leu Asp Ser Gly Pro Arg Lys Arg
      210      215      220
Pro Thr Ser Ala Ser Ser Ser Pro Glu Pro Pro Glu Phe Ser Thr Phe
      225      230      235      240
Arg Ala Cys Gln

```

```

<210> 703
<211> 255
<212> PRT
<213> Mouse

```

```

<400> 703
Met Ala Gln Leu Ala Arg Ala Thr Arg Ser Pro Leu Ser Trp Leu Leu
1      5      10      15
Leu Leu Phe Cys Tyr Ala Leu Arg Lys Ala Gly Gly Asp Ile Arg Val
      20      25      30
Leu Val Pro Tyr Asn Ser Thr Gly Val Leu Gly Gly Ser Thr Thr Leu
      35      40      45
His Cys Ser Leu Thr Ser Asn Glu Asn Val Thr Ile Thr Gln Ile Thr
      50      55      60
Trp Met Lys Lys Asp Ser Gly Gly Ser His Ala Leu Val Ala Val Phe
      65      70      75      80
His Pro Lys Lys Gly Pro Asn Ile Lys Glu Pro Glu Arg Val Lys Phe
      85      90      95
Leu Ala Ala Gln Gln Asp Leu Arg Asn Ala Ser Leu Ala Ile Ser Asn
      100      105      110
Leu Ser Val Glu Asp Glu Gly Ile Tyr Glu Cys Gln Ile Ala Thr Phe
      115      120      125
Pro Arg Gly Ser Arg Ser Thr Asn Ala Trp Leu Lys Val Gln Ala Arg
      130      135      140
Pro Lys Asn Thr Ala Glu Ala Leu Glu Pro Ser Pro Thr Leu Ile Leu
      145      150      155      160
Gln Asp Val Ala Lys Cys Ile Ser Ala Asn Gly His Pro Pro Gly Arg
      165      170      175
Ile Ser Trp Pro Ser Asn Val Asn Gly Ser His Arg Glu Met Lys Glu
      180      185      190
Pro Gly Ser Gln Pro Gly Thr Thr Val Thr Ser Tyr Leu Ser Met
      195      200      205

```

Val Pro Ser Arg Gln Ala Asp Gly Lys Asn Ile Thr Cys Thr Val Glu  
 210 215 220  
 His Glu Ser Leu Gln Glu Leu Asp Gln Leu Leu Val Thr Leu Ser Gln  
 225 230 235 240  
 Pro Tyr Pro Pro Glu Asn Val Ser Ile Ser Gly Tyr Asp Gly Asn  
 245 250 255

<210> 704  
 <211> 255  
 <212> PRT  
 <213> Mouse

<400> 704  
 Met Phe Leu Val Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ala His  
 1 5 10 15  
 Ser Thr Ala Gln Leu Ala Gly Leu Pro Leu Pro Leu Gly Gln Gly Pro  
 20 25 30  
 Pro Leu Pro Leu Asn Gln Gly Pro Leu Pro Leu Asn Gln Gly Gln  
 35 40 45  
 Leu Leu Pro Leu Ala Gln Gly Leu Pro Leu Ala Val Ser Pro Ala Leu  
 50 55 60  
 Pro Ser Asn Pro Thr Asp Leu Leu Ala Gly Lys Phe Thr Asp Ala Leu  
 65 70 75 80  
 Ser Gly Gly Leu Leu Ser Gly Gly Leu Leu Gly Ile Leu Glu Asn Ile  
 85 90 95  
 Pro Leu Leu Asp Val Ile Lys Ser Gly Gly Gly Asn Ser Asn Gly Leu  
 100 105 110  
 Val Gly Gly Leu Leu Gly Lys Leu Thr Ser Ser Val Pro Leu Leu Asn  
 115 120 125  
 Asn Ile Leu Asp Ile Lys Ile Thr Asp Pro Gln Leu Leu Glu Leu Gly  
 130 135 140  
 Leu Val Gln Ser Pro Asp Gly His Arg Leu Tyr Val Thr Ile Pro Leu  
 145 150 155 160  
 Gly Leu Thr Leu Asn Val Asn Met Pro Val Val Gly Ser Leu Leu Gln  
 165 170 175  
 Leu Ala Val Lys Leu Asn Ile Thr Ala Glu Val Leu Ala Val Lys Asp  
 180 185 190  
 Asn Gln Gly Arg Ile His Leu Val Leu Gly Asp Cys Thr His Ser Pro  
 195 200 205  
 Gly Ser Leu Lys Ile Ser Leu Leu Asn Gly Val Thr Pro Val Gln Ser  
 210 215 220  
 Phe Leu Asp Asn Leu Thr Gly Ile Leu Thr Lys Val Leu Pro Glu Leu  
 225 230 235 240  
 Ile Gln Gly Lys Val Cys Pro Leu Val Asn Gly Ile Leu Ser Gly  
 245 250 255

<210> 705  
 <211> 255  
 <212> PRT  
 <213> Mouse

<400> 705  
 Met Ala Thr Thr Thr Cys Gln Val Val Gly Leu Leu Leu Ser Leu Leu  
 1 5 10 15  
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr  
 20 25 30  
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ala Val Phe Gln His Glu Gly



```

      35      40      45
Leu Trp Arg Ser Cys Val Gln Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50      55      60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Val Ile Gly Ile Leu Val
      85      90      95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Asp Asp Ser
      100      105      110
Ala Lys Ala Lys Met Thr Leu Thr Ser Gly Ile Leu Phe Ile Ile Ser
      115      120      125
Gly Ile Cys Ala Ile Ile Gly Val Ser Val Phe Ala Asn Met Leu Val
      130      135      140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Ser Gly Met Gly Gly
145      150      155      160
Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala
      165      170      175
Ala Leu Phe Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly
      180      185      190
Val Met Met Cys Ile Ala Cys Arg Gly Leu Thr Pro Asp Asp Ser Asn
      195      200      205
Phe Lys Ala Val Ser Tyr His Ala Ser Gly Gln Asn Val Ala Tyr Arg
      210      215      220
Pro Gly Gly Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Arg Asn
225      230      235      240
Lys Lys Ile Tyr Asp Gly Gly Ala Arg Thr Glu Asp Asp Glu Gln
      245      250      255

```

&lt;210&gt; 706

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 706

```

Met Gly Arg Phe Ala Ala Ala Leu Val Gly Ser Leu Phe Trp Leu Gly
 1      5      10      15
Leu Leu Leu Cys Gly Leu Gly Ser Leu Ala Ser Ala Glu Pro Arg Ala
      20      25      30
Pro Pro Asn Arg Ile Ala Ile Val Gly Ala Gly Ile Gly Gly Thr Ser
      35      40      45
Ser Ala Tyr Tyr Leu Arg Lys Phe Gly Lys Asp Val Lys Ile Asp
      50      55      60
Val Phe Glu Arg Glu Glu Val Gly Gly Arg Leu Ala Thr Leu Lys Val
      65      70      75      80
Gln Gly His Asp Tyr Glu Ala Gly Gly Ser Val Ile His Pro Leu Asn
      85      90      95
Leu His Met Lys Arg Phe Val Lys Glu Leu Gly Leu Ser Ser Val Pro
      100      105      110
Ala Ser Gly Gly Leu Val Gly Val Tyr Asn Gly Lys Ser Leu Val Phe
      115      120      125
Glu Glu Ser Ser Trp Phe Val Ile Asn Val Ile Lys Leu Val Trp Arg
      130      135      140
Tyr Gly Phe Gln Ser Leu Arg Met His Met Trp Val Glu Asp Leu Leu
145      150      155      160
Asp Lys Phe Met Arg Ile Tyr Arg Tyr Gln Ser His Asp Tyr Ala Phe
      165      170      175
Ser Ser Val Glu Lys Leu Met His Ala Ile Gly Gly Asp Asp Tyr Val

```

```

      180      185      190
Arg Leu Leu Asn Gln Thr Leu Arg Glu Asn Leu Lys Lys Ala Gly Phe
      195      200      205
Ser Glu Thr Phe Leu Asn Glu Met Ile Ala Pro Val Met Lys Val Asn
      210      215      220
Tyr Gly Gln Ser Thr Asp Ile Asn Ala Phe Val Gly Ala Val Ser Leu
225      230      235      240
Thr Ala Ala Asp Ser Asn Leu Trp Ala Val Glu Gly Gly Asn Lys
      245      250      255

```

<210> 707  
 <211> 150  
 <212> PRT  
 <213> Mouse

```

<400> 707
Met Ser Trp Trp Arg Asp Asn Phe Trp Ile Ile Leu Ala Met Ser Ile
 1      5      10      15
Ile Phe Ile Ser Leu Val Leu Gly Leu Ile Leu Tyr Cys Val Cys Arg
      20      25      30
Trp Gln Leu Arg Gln Gly Arg Asn Trp Glu Ile Ala Lys Pro Ser Lys
      35      40      45
Gln Asp Gly Arg Asp Glu Glu Lys Met Tyr Glu Asn Val Leu Asn Ser
      50      55      60
Ser Pro Gly Gln Leu Pro Ala Leu Pro Pro Arg Gly Ser Pro Phe Pro
65      70      75      80
Gly Asp Leu Ala Pro Gln Glu Ala Pro Arg Gln Pro Ser Ala Trp Tyr
      85      90      95
Ser Ser Val Lys Lys Val Arg Asn Lys Lys Val Phe Ala Ile Ser Gly
      100      105      110
Ser Thr Glu Pro Glu Asn Asp Tyr Asp Asp Val Glu Ile Pro Ala Thr
      115      120      125
Thr Glu Thr Gln His Ser Lys Thr Thr Pro Phe Trp Gln Ala Glu Val
      130      135      140
Gly Leu His Ser Ser Phe
145      150

```

<210> 708  
 <211> 114  
 <212> PRT  
 <213> Mouse

```

<400> 708
Met Phe Leu Val Tyr Phe Ser Arg Arg Gly His Cys Ile Asn Tyr Val
 1      5      10      15
Lys Gly His Ala Asp Ser Leu Ala Pro Trp Cys Cys Gly Val Gly Leu
      20      25      30
Arg Ser Pro Leu Ala Arg Pro Gln His Gly His Val Ser Pro Lys Asp
      35      40      45
His Val Pro Gly Gly His Ala Pro Gly Pro Ser His Lys Trp Leu Cys
      50      55      60
Thr Ala Ala Leu Trp Arg Tyr Leu Glu His Ser Ala Val Thr His Gly
65      70      75      80
Thr Ala Leu Pro Glu Ala His Ala Val Arg Gly Lys His Gly Lys Lys
      85      90      95
Gly Arg Arg Val Val Cys Cys Ser Val Asp Phe Pro Gln Ala Thr Ser
      100      105      110

```

Leu Phe

<210> 709  
 <211> 132  
 <212> PRT  
 <213> Mouse

<400> 709  
 Ala His Pro Arg Pro Gly Ala Arg Arg Pro Arg Leu Leu Ala Phe Gln  
 1 5 10 15  
 Ala Ser Cys Ala Pro Ala Pro Gly Ser Arg Asp Arg Cys Pro Glu Glu  
 20 25 30  
 Gly Gly Pro Arg Cys Leu Arg Val Tyr Ala Gly Leu Ile Gly Thr Val  
 35 40 45  
 Val Thr Pro Asn Tyr Leu Asp Asn Val Ser Ala Arg Val Ala Pro Trp  
 50 55 60  
 Cys Gly Cys Ala Ala Ser Gly Asn Arg Arg Glu Glu Cys Glu Ala Phe  
 65 70 75 80  
 Arg Lys Leu Phe Thr Arg Asn Pro Cys Leu Asp Gly Ala Ile Gln Ala  
 85 90 95  
 Phe Asp Ser Leu Gln Pro Ser Val Leu Gln Asp Gln Thr Ala Gly Cys  
 100 105 110  
 Cys Phe Pro Arg Val Ser Trp Leu Tyr Ala Leu Thr Ala Leu Ala Leu  
 115 120 125  
 Gln Ala Leu Leu  
 130

<210> 710  
 <211> 255  
 <212> PRT  
 <213> Mouse

<400> 710  
 Met Arg Val Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe  
 1 5 10 15  
 Gly Phe Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu  
 20 25 30  
 Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val  
 35 40 45  
 Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser  
 50 55 60  
 Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala  
 65 70 75 80  
 Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn  
 85 90 95  
 Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu  
 100 105 110  
 Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ala Gly  
 115 120 125  
 Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu  
 130 135 140  
 Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val  
 145 150 155 160  
 Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn  
 165 170 175  
 Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile

				180					185				190			
Gly	Gln	Phe	Gly	Val	Gly	Phe	Tyr	Ser	Ala	Phe	Leu	Val	Ala	Asp	Lys	
		195					200					205				
Val	Ile	Val	Thr	Ser	Lys	His	Asn	Asn	Asp	Thr	Gln	His	Ile	Trp	Glu	
	210					215					220					
Ser	Asp	Ser	Asn	Glu	Phe	Ser	Val	Ile	Ala	Asp	Pro	Arg	Gly	Asn	Thr	
225					230					235					240	
Leu	Gly	Arg	Gly	Thr	Thr	Ile	Thr	Leu	Val	Leu	Lys	Glu	Glu	Ala		
				245				250						255		

```
<210> 711
<211> 224
<212> PRT
<213> Mouse
```

<400> 711															
Met	Ala	Leu	Leu	Ile	Ser	Leu	Pro	Gly	Gly	Thr	Pro	Ala	Met	Ala	Gln
1				5					10					15	
Val	Leu	Leu	Leu	Leu	Ser	Ser	Gly	Cys	Leu	His	Ala	Gly	Asn	Ser	Glu
			20					25					30		
Arg	Tyr	Asn	Arg	Lys	Asn	Gly	Phe	Gly	Val	Asn	Gln	Pro	Glu	Arg	Cys
		35					40					45			
Ser	Gly	Val	Gln	Gly	Gly	Ser	Ile	Asp	Ile	Pro	Phe	Ser	Phe	Tyr	Phe
	50					55					60				
Pro	Trp	Lys	Leu	Ala	Lys	Asp	Pro	Gln	Met	Ser	Ile	Ala	Trp	Lys	Trp
65					70					75					80
Lys	Asp	Phe	His	Gly	Glu	Val	Ile	Tyr	Asn	Ser	Ser	Leu	Pro	Phe	Ile
				85					90					95	
His	Glu	His	Phe	Lys	Gly	Arg	Leu	Ile	Leu	Asn	Trp	Thr	Gln	Gly	Gln
			100					105					110		
Thr	Ser	Gly	Val	Leu	Arg	Ile	Leu	Asn	Leu	Lys	Glu	Ser	Asp	Gln	Ala
		115					120					125			
Gln	Tyr	Phe	Ser	Arg	Val	Asn	Leu	Gln	Ser	Thr	Glu	Gly	Met	Lys	Leu
	130					135					140				
Trp	Gln	Ser	Ile	Pro	Gly	Thr	Gln	Leu	Asn	Val	Thr	Gln	Ala	Leu	Asn
145					150					155				160	
Thr	Thr	Met	Arg	Ser	Pro	Phe	Ile	Val	Thr	Ser	Glu	Phe	Thr	Thr	Ala
				165					170					175	
Gly	Leu	Glu	His	Thr	Ser	Asp	Gln	Arg	Asn	Pro	Ser	Leu	Met	Asn	Leu
			180					185					190		
Gly	Ala	Met	Val	Thr	Met	Leu	Leu	Ala	Lys	Val	Leu	Val	Ile	Val	Leu
		195					200					205			
Val	Tyr	Gly	Trp	Met	Ile	Phe	Leu	Arg	Trp	Lys	Gln	Arg	Pro	Ala	His
	210					215					220				

```
<210> 712
<211> 133
<212> PRT
<213> Mouse
```

<400> 712															
Met	Ala	Leu	Pro	Trp	Thr	Ile	Leu	Leu	Ala	Leu	Ser	Gly	Ile	Tyr	Val
1				5					10					15	
Gln	Gly	Ala	Gln	Ala	Trp	Cys	Ser	Glu	Glu	Asp	Thr	Leu	Glu	Leu	Asp
		20						25					30		
Lys	Leu	Val	Ser	Glu	Pro	Asp	Ile	Val	Lys	Phe	Ala	Leu	Ser	Ala	Phe
		35					40						45		

```

His Lys Lys Ser Lys Asp Glu Tyr Ala Tyr Arg Val Ile His Ile Met
 50      55      60
Asn Phe Leu Lys Val Gln Glu Glu Pro Pro Gln Thr Phe Phe Val Lys
65      70      75      80
Leu Arg Leu Thr Arg Thr Ile Cys Met Lys Phe Glu Lys Ser Leu Asp
      85      90      95
Thr Cys Pro Leu Pro Glu Leu Gln Asn Ile Leu Ile Cys Ser Phe Ser
      100      105      110
Ile Ser Ser Pro Gly Ser Lys Gln Phe Asn Leu Leu Lys Met Thr Cys
      115      120      125
Ser Glu Gly Leu Leu
      130

```

<210> 713  
 <211> 255  
 <212> PRT  
 <213> Mouse

```

<400> 713
Glu Glu Glu Asp Leu Arg Arg Arg Leu Lys Tyr Phe Phe Met Ser Pro
 1      5      10      15
Cys Asp Lys Phe Arg Ala Lys Gly Arg Lys Pro Cys Lys Leu Met Leu
      20      25      30
Gln Val Val Lys Ile Leu Val Val Thr Val Gln Leu Ile Leu Phe Gly
      35      40      45
Leu Ser Asn Gln Leu Val Val Thr Phe Arg Glu Glu Asn Thr Ile Ala
      50      55      60
Phe Arg His Leu Phe Leu Leu Gly Tyr Ser Asp Gly Ser Asp Asp Thr
      65      70      75      80
Phe Ala Ala Tyr Thr Gln Glu Gln Leu Tyr Gln Ala Ile Phe Tyr Ala
      85      90      95
Val Asp Gln Tyr Leu Ile Leu Pro Glu Ile Ser Leu Gly Arg Tyr Ala
      100      105      110
Tyr Val Arg Gly Gly Gly Gly Pro Trp Ala Asn Gly Ser Ala Leu Ala
      115      120      125
Leu Cys Gln Arg Tyr Tyr His Arg Gly His Val Asp Pro Ala Asn Asp
      130      135      140
Thr Phe Asp Ile Asp Pro Arg Val Val Thr Asp Cys Ile Gln Val Asp
      145      150      155      160
Pro Pro Asp Arg Pro Pro Asp Ile Pro Ser Glu Asp Leu Asp Phe Leu
      165      170      175
Asp Gly Ser Ala Ser Tyr Lys Asn Leu Thr Leu Lys Phe His Lys Leu
      180      185      190
Ile Asn Val Thr Ile His Phe Gln Leu Lys Thr Ile Asn Leu Gln Ser
      195      200      205
Leu Ile Asn Asn Glu Ile Pro Asp Cys Tyr Thr Phe Ser Ile Leu Ile
      210      215      220
Thr Phe Asp Asn Lys Ala His Ser Gly Arg Ile Pro Ile Arg Leu Glu
      225      230      235      240
Thr Lys Thr His Ile Gln Glu Cys Lys His Pro Ser Val Ser Arg
      245      250      255

```

<210> 714  
 <211> 255  
 <212> PRT  
 <213> Mouse

&lt;400&gt; 714

```

Met Asn Ile Val Val Glu Phe Phe Val Val Thr Phe Lys Val Leu Trp
 1          5          10          15
Ala Phe Val Leu Ala Ala Ala Arg Trp Leu Val Arg Pro Lys Glu Lys
 20          25          30
Ser Val Ala Gly Gln Val Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu
 35          40          45
Gly Arg Leu Phe Ala Leu Glu Phe Ala Arg Arg Arg Ala Leu Leu Val
 50          55          60
Leu Trp Asp Ile Asn Thr Gln Ser Asn Glu Glu Thr Ala Gly Met Val
 65          70          75          80
Arg His Ile Tyr Arg Asp Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln
 85          90          95
Ala Gly Lys Gly Glu Glu Glu Ile Leu Pro Pro Cys Asn Leu Gln Val
100          105          110
Phe Thr Tyr Thr Cys Asp Val Gly Lys Arg Glu Asn Val Tyr Leu Thr
115          120          125
Ala Glu Arg Val Arg Lys Glu Val Gly Glu Val Ser Val Leu Val Asn
130          135          140
Asn Ala Gly Val Gly Ser Gly His His Leu Leu Glu Cys Pro Asp Glu
145          150          155          160
Leu Ile Glu Arg Thr Met Met Val Asn Cys His Ala His Phe Trp Thr
165          170          175
Thr Lys Ala Phe Leu Pro Thr Met Leu Glu Ile Asn His Gly His Ile
180          185          190
Val Thr Val Ala Ser Ser Leu Gly Leu Phe Ser Thr Ala Gly Val Glu
195          200          205
Asp Tyr Cys Ala Ser Lys Phe Gly Val Val Gly Phe His Glu Ser Leu
210          215          220
Ser His Glu Leu Lys Ala Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu
225          230          235          240
Val Cys Pro Tyr Leu Val Asp Thr Gly Met Phe Arg Gly Cys Arg
245          250          255

```

&lt;210&gt; 715

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 715

```

Met Phe Pro Lys Asn Ser Arg Cys Pro Thr Cys Asp Leu Arg Lys Pro
 1          5          10          15
Ala Arg Ser Lys His Cys Arg Leu Cys Asp Arg Cys Val His Arg Phe
 20          25          30
Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Thr
 35          40          45
Arg Tyr Phe Leu Ile Tyr Leu Leu Thr Leu Thr Ala Ser Ala Ala Thr
 50          55          60
Ile Ala Thr Val Thr Ala Ala Phe Leu Leu Arg Leu Val Thr Val Ser
 65          70          75          80
Asp Leu Tyr Gln Glu Thr Tyr Leu Asp Asp Val Gly His Phe Gln Ala
 85          90          95
Val Asp Thr Val Phe Leu Ile Gln His Leu Phe Leu Ala Phe Pro Arg
100          105          110
Ile Val Phe Leu Leu Gly Phe Val Ile Val Leu Ser Met Leu Leu Ala
115          120          125
Gly Tyr Leu Cys Phe Ala Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr

```

130 135 140  
 Asn Glu Trp Tyr Lys Gly Asp Trp Ala Trp Cys Gln Arg Trp Pro Leu  
 145 150 155 160  
 Val Ala Trp Ser Pro Ser Ala Glu Pro Arg Ile His Gln Asn Ile His  
 165 170 175  
 Ser His Gly Phe Arg Ser Asn Leu Arg Glu Ile Phe Leu Pro Ala Thr  
 180 185 190  
 Pro Ser Tyr Lys Lys Lys Glu Lys  
 195 200

<210> 716  
 <211> 115  
 <212> PRT  
 <213> Mouse

<400> 716  
 Gly Glu Leu Arg Ala Leu Leu Ala Phe Thr His Leu Ser Ser Ala His  
 1 5 10 15  
 Phe Trp Leu Met Met Thr Leu Gly Gly Leu Phe Gly Phe Ala Ile Gly  
 20 25 30  
 Tyr Val Thr Gly Leu Leu Ile Lys Phe Thr Ser Pro Leu Thr His Asn  
 35 40 45  
 Val Ser Gly Thr Ala Lys Ala Cys Ala Gln Thr Val Leu Ala Val Leu  
 50 55 60  
 Tyr Tyr Glu Glu Ile Lys Ser Phe Leu Trp Trp Thr Ser Asn Leu Met  
 65 70 75 80  
 Val Leu Gly Gly Ser Ser Ala Tyr Thr Trp Val Arg Gly Trp Glu Met  
 85 90 95  
 Gln Lys Thr Gln Glu Asp Pro Ser Ser Lys Asp Gly Glu Lys Ser Ala  
 100 105 110  
 Ile Arg Val  
 115

<210> 717  
 <211> 88  
 <212> PRT  
 <213> Mouse

<400> 717  
 Met Lys Ile Pro Ile Leu Pro Val Val Ala Leu Leu Ser Leu Leu Ala  
 1 5 10 15  
 Leu His Ala Val Gln Gly Ala Ala Leu Gly His Pro Thr Ile Tyr Pro  
 20 25 30  
 Glu Asp Ser Ser Tyr Asn Asn Tyr Pro Thr Ala Thr Glu Ala Phe Gln  
 35 40 45  
 Ser Glu Asn Phe Leu Asn Trp His Val Ile Thr Asp Met Phe Lys Asn  
 50 55 60  
 Ala Phe Pro Phe Ile Asn Trp Asp Phe Phe Pro Lys Val Lys Gly Leu  
 65 70 75 80  
 Arg Ser Ala Ala Pro Asp Ser Gln  
 85

<210> 718  
 <211> 84  
 <212> PRT  
 <213> Mouse

&lt;400&gt; 718

```

Met Arg Leu Pro Ile Phe His Ile Ile Ala Phe Phe Phe Leu Val Val
 1           5           10           15
Ser Met Gly Cys Thr Cys Ala His Gly Gly Gln Arg Ser Asp Leu Cys
           20           25           30
Thr Cys Gly Tyr Met Glu Val Arg Gly His Val Arg Arg Leu Leu Leu
           35           40           45
Leu Phe Ser Thr Phe Lys Arg Ile Val Ile Glu Ala Glu Gly Gly Gly
 50           55           60
Met Gly Trp Gly Gly Leu Gln Arg Gly Asn Arg Glu Gly Gly Gln His
65           70           75           80
Leu Lys Cys Lys

```

&lt;210&gt; 719

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 719

```

Met Phe Val Ala Phe Tyr Ile Cys Thr Phe Leu Met Arg Phe Val Ser
 1           5           10           15
Thr Pro Val Thr Arg Met Cys Cys Pro Arg Gly Asp Ala Ala Trp Arg
           20           25           30
Arg Pro Tyr Pro Leu Pro Leu Asp Leu Phe Gly Gly Thr Pro Ser Pro
           35           40           45
Gly Pro Gly Ala Gly Arg Gly Ala Ser Cys Arg Pro Gln Ala Tyr Ser
 50           55           60
Glu Leu Val Phe Leu Lys Val Phe Leu Asp Pro Val Leu Val Asn Ile
65           70           75           80
Ser Ile Ile Leu Thr Arg Ala Ser Ser Cys Ser Leu Ser Leu Ser Leu
           85           90           95
Ser Leu Ser Leu Phe Asn Phe Ile Ile Ile Leu Ala Thr Cys Thr Phe
           100           105           110
Leu Thr Lys Phe Ile Val Ala Ile Lys Val Phe Tyr Phe Pro Val His
           115           120           125
Ile Thr Leu Val Ser Ser Pro
           130           135

```

&lt;210&gt; 720

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 720

```

Met Ile Arg Ile Phe Val Leu Phe Val Phe Trp Phe Leu Ile Tyr Asn
 1           5           10           15
Ser Pro Thr His Leu Tyr Leu Phe Ile Phe Phe Ser Leu Phe Leu Gly
           20           25           30
Lys Pro Asp Leu Leu His Pro Gln Ala Ile Pro Pro Ala Ser Leu Gly
           35           40           45
Gly Pro Leu Leu Gly Leu Pro Cys Ala Pro Val Cys Pro Gly Leu Ala
 50           55           60
Arg Leu Ser Pro Pro Ala Arg Gly Ser Ser Arg Ala Leu Met Val Leu
65           70           75           80
Lys Pro Ala Pro Leu Pro Tyr Val Leu His Phe Leu Gly Pro Val Pro
           85           90           95

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 115 120 125  
 Lys

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 20 25 30  
 Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu  
 35 40 45  
 Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu  
 50 55 60  
 Glu Leu Ala Phe Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
 65 70 75 80  
 Ala Arg Arg Ala Gln Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu  
 85 90 95  
 Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu  
 100 105 110  
 Thr Asp Thr Ser Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu  
 115 120 125  
 Phe Gly Lys Ile Asp Ile Leu Val Asn Asn Gly Gly Arg Ser Gln Arg  
 130 135 140  
 Ser Leu Val Leu Glu Thr Asn Leu Asp Val Phe Lys Glu Leu Ile Asn  
 145 150 155 160  
 Leu Asn Tyr Ile Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His  
 165 170 175  
 Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Ala  
 180 185 190  
 Gly Ile Ala Ser Val Ser Leu Ser Ser Gly Tyr Cys Ala Ser Lys His  
 195 200 205  
 Ala Leu Arg Gly Phe Phe Asn Ala Leu His Ser Glu Leu Gly Gln Tyr  
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 Pro Gly Ile Thr Phe Cys Asn Val Tyr Pro Gly Pro Val Gln Ser Asp  
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 <213> Mouse

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 20 25 30  
 Ser Thr Ser Phe Phe Ile Ala Leu Val Val Phe Tyr Ile Leu Phe Cys

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      35      40      45
Leu Leu Trp Pro Arg Ile Val Lys Ala Trp Val Ser Phe Arg Trp Lys
  50      55      60
Ile His Asn Met Met Ala Pro Glu Thr Tyr Ser Ser Ser Ser Ser
  65      70      75      80
Gly Gly Phe Thr Leu His Ser His Ser Ser Glu Gly Ser Phe Glu Gly
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Lys Val Ala
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 <213> Human

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      20      25      30
Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
      35      40      45
Phe Phe Ser Gly Ile Val Gly Gly Leu Leu Met Leu Leu Pro Ala
      50      55      60
Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
      65      70      75      80
His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
      85      90      95
Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
      100      105      110
Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
      115      120      125
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Ala
      145

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<210> 724  
 <211> 217  
 <212> PRT  
 <213> Mouse

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      20      25      30
Arg Arg Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser
      35      40      45
Gly Ser Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu
      50      55      60
Leu Ser Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg
      65      70      75      80
Gln Pro Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp
      85      90      95

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Phe Ile Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala
      100      105      110
Glu Glu Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu
      115      120      125
Lys Pro Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg
      130      135      140
Arg Pro Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln
      145      150      155      160
Gln Gln Ser Gly Gly Trp Gly Ser Pro Arg Lys Asp Ser Val Leu Lys
      165      170      175
Arg Gly Ile Arg Ala Ala Gly Ala Gly Ala Ser Ala Pro Ser Thr Gln
      180      185      190
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Gln Val Leu Pro Leu Gln Ser Leu Phe
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<210> 725
<211> 255
<212> PRT
<213> Mouse

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Leu Leu Leu Leu Val Val Gly Phe Leu Phe Gly Arg Asp Pro
      20      25      30
Asp Tyr Gly Leu Gly Thr Thr Ala Thr Leu Asp Glu Asp Pro Tyr Arg
      35      40      45
Ser Arg Asn Leu Ser Ala Ser Ser Pro Gln Leu Leu Pro Pro Lys
      50      55      60
Cys Glu Met Leu His Val Ala Ile Val Cys Ala Gly Tyr Asn Ser Ser
      65      70      75      80
Arg Glu Ile Ile Thr Leu Thr Lys Ser Leu Leu Phe Tyr Arg Lys Asn
      85      90      95
Pro Leu His Leu His Leu Ile Thr Asp Ala Val Ala Arg Asn Ile Leu
      100      105      110
Glu Thr Leu Phe Arg Thr Trp Met Val Pro Ala Val Val Val Ser Phe
      115      120      125
Tyr Asp Ala Glu Glu Leu Lys Pro Leu Val Ser Trp Ile Pro Asn Lys
      130      135      140
His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu Val Leu Pro Ser Ile
      145      150      155      160
Leu Pro Pro Ser Leu Ala Arg Val Ile Val Leu Asp Thr Asp Val Thr
      165      170      175
Phe Ser Ser Asp Ile Val Glu Leu Trp Ala Leu Phe Asp His Phe Ser
      180      185      190
Asp Lys Gln Val Val Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr Leu
      195      200      205
Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu Gly Arg Gly
      210      215      220
Phe Asn Thr Gly Val Ile Leu Leu Trp Leu Asp Arg Leu Gln Gln Thr
      225      230      235      240
Gly Trp Glu Gln Met Trp Lys Val Thr Ala Lys Arg Glu Leu Leu
      245      250      255

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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ01/00099

<b>A. CLASSIFICATION OF SUBJECT MATTER</b>												
Int. Cl. <sup>7</sup> : C12N 15/12, 15/18, 15/19												
According to International Patent Classification (IPC) or to both national classification and IPC												
<b>B. FIELDS SEARCHED</b>												
Minimum documentation searched (classification system followed by classification symbols) AS BELOW												
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched AS BELOW.												
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Dgene, Swiss Prot, EMBL, Genbank, : SEQ ID. NOS. 1 - 10.												
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>												
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.										
P, X	EP 1 067 182 HELIX RESEARCH INSTITUTE (10 January 2001) See Sequence Id. 487, & GeneBank Accession Number AX136565.	1 - 3. (SEQ ID NO 1)										
P, X	EP 1067 182 HELIX RESEARCH INSTITUTE (10 January 2001) See Sequence Id. 219, & GeneBank Accession Number AX136297.	1 - 3. (SEQ ID NO 1)										
X	EMBL Accession Number AC008119 (9 October 1999) Homo sapiens 12q24.1-116.6-118.9 BAC RPC11-951111	1 - 3. (SEQ ID NO 1)										
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex												
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td>"A" document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E" earlier application or patent but published on or after the international filing date</td> <td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O" document referring to an oral disclosure, use, exhibition or other means</td> <td>"&amp;" document member of the same patent family</td> </tr> <tr> <td>"P" document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	"P" document published prior to the international filing date but later than the priority date claimed	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention											
"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone											
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art											
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family											
"P" document published prior to the international filing date but later than the priority date claimed												
Date of the actual completion of the international search 20 August 2001		Date of mailing of the international search report 21 SEPTEMBER 2001										
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustalia.gov.au Facsimile No. (02) 6285 3929		Authorized officer  ALISTAIR BESTOW Telephone No : (02) 6283 2450										

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ01/00099

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US, A, 5 952 486 L. N. BLOKSBERG ET. AL. (14 September 1999) See SEQ ID 53. & GeneBank Accession number AR074144.	1 - 3. (SEQ ID NO 2)
X	WO, A, 2000 40752 THE NOTTINGHAM TRENT UNIVERSITY (13 July 2000) See SEQ ID NO. 2. & GeneBank Accession Number AX026540.	1 - 3. (SEQ ID NO 2)
X	EMBL Accession Number UCAJ4935 (2 March 1999.) Urechis caupo mRNA for cytoplasmic intermediate filament protein.	1 - 3. (SEQ ID NO 2)
X	WO, A, 99 53040 METAGEN GESELLSCHAFT FÜR GENOMFORSCHUNG MBH (21 October 1999) See SEQ ID 31. & GenBank Accession Number AX014842.	1 - 3. (SEQ ID NO 4)
P, X	WO, A, 2001 07612 INCYTE GENOMICS, INC. (1 February 2001) See SEQ ID 43 & Genebank Accession Number AX078375.	1 - 3. (SEQ ID NO 4)
P, X	WO, A, 2001 10902 CURAGEN CORPORATION (15 February 2001) See SEQ ID 5 & Genebank Accession Number AX084211.	1 - 3. (SEQ ID NO 5)
X	EMBL Accession Number AF169677 (29 JANUARY 2000) Homo sapiens leucine-rich repeat transmembrane protein FLRT3 (FLRT3) mRNA, complete cds.	1 - 3. (SEQ ID NO 5)
X	EMBL Accession Number RNMOG (20 August 1992) Rattus norvegicus myelin/oligodendrocyte glycoprotein (MOG) gene, complete cds.	1 - 3. (SEQ ID NO 7)
A	EMBL Accession Number D50030 (14 April 2000) Homo sapiens gene for hepatocyte growth factor activator, complete cds.	1 - 3. (SEQ ID NO 8)
X	WO, A, 99 55865 GENESIS RESEARCH AND DEVELOPMENT CORPORATION LIMITED (4 November 1999) See SEQ ID NOS 1 - 10, 147, 187, 196, 294, 295 and 395.	1 - 3, 8-17, 27-29 (SEQ ID NOS 1-10, 147, 196, 294, 295, 413-5, 417)
P, X	WO, A, 2000 69884 GENESIS RESEARCH AND DEVELOPMENT CORPORATION LIMITED (23 November 2000) See SEQ ID NOS 1 - 10, 147, 187, 196, 294, 295 and 395.	1 - 3, 8-17, 27-29 (SEQ ID NOS 1-10, 147, 196, 294, 295, 413-5, 417)

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/NZ01/00099

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO, A, 00 63230 HUMAN GENOME SCIENCES, INC. (26 October 2000) See SEQ ID NO 68 and pages 16-29	1-3, 8-17, 27-29 (SEQ ID NOS 196, 413-5, 417)
X	WO, A, 00 29438 MILLENNIUM PHARMACEUTICALS, INC. (25 May 2000) See Figures 1, 3, 5, 7 and 8	1-3, 8-17, 27-29 (SEQ ID NOS 196, 413-5, 417)
PX	WO, A, 00 63377 ZYMOGENETICS, INC. (26 October 2000) See SEQ ID NOS 1 and 11	1-3 (SEQ ID NO 147, 294)
PX	WO, A, 01 49728 PROTOGENE, INC. (12 July 2001) See SEQ ID NO 59 and Table 1	1-3 (SEQ ID NO 147)
PX	WO, A, 00 73448 ZYMOGENETICS, INC. (7 December 2000) See SEQ ID NOS 1 and 14	1-3 (SEQ ID NO 294)
X	GenPept Accession No. CAB53702 (18 February 2000) Hypothetical Protein <i>Homo sapiens</i> Ottenwaelder B et al	1-3 (SEQ ID NO 295)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ01/00099

**Box I** Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos :  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos :  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

**Box II** Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:  
1-3, 8-17 and 27-29 (SEQ ID NOS 1-10, 147, 196, 294, 295, 413-415, 417)  
More than one invention has been claimed. (*continued in supplemental box*)
4. ☐ No required additional search fees were timely paid by the applicant.

**Remark on Protest**

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

**Supplemental Box**

(To be used when the space in any of Boxes I to VIII is not sufficient)

**Continuation of Box No: II**

Rule 13.1 of the PCT states the principle that an International Application should relate to only one invention or, if there is more than one invention, that the inclusion of those inventions in one International Application is only permitted if all inventions are so linked to form a single general inventive concept. Rule 13.2 of the PCT defines the method for determining whether the requirement of unity of invention is satisfied in respect of a group of inventions claimed in the International application. Unity of invention exists only when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding "special technical features." The expression "special technical features" is defined in Rule 13.2 as meaning those technical features that define a contribution which each of the inventions, considered as a whole, makes over the prior art. The determination is made on the contents of the claims as interpreted in the light of the description and drawings (if any).

There is no special technical feature which is common to all 725 sequences disclosed in the specification. It is well known in the art that for a given cell type, the cell will express a great many sequences, each having a different function from the others. That they are sourced from skin cells is not a special technical feature. For applications claiming nucleotides and peptides, there are two features which are to be considered for the purposes of determining the number of inventions in a specification.

1) If the polynucleotide has a corresponding peptide, then the two sequences may have a common special technical feature because the nucleotide encodes the peptide. Therefore they are regarded as a single invention.

In the present case, the specification does not disclose a complete concordance between the polynucleotides and corresponding polypeptides, other than those disclosed in Table 2. While Table 2 purports to provide a concordance between nucleotides and peptides for which they code, this is incomplete, as the majority of sequences are not referred to on this table. Therefore the ISA is unable to confidently determine the number of inventions, on the basis of a concordance between the polynucleotides and the peptides.

2) A group of two or more nucleotides, or two or more peptides, which share a significant structural element. A "significant structural element" is the structural element that defines the specific biological activity of an amino acid sequence or a nucleotide sequence or its encoded polypeptide and is disclosed as the feature that defines the contribution which each of the inventions, considered as a whole, makes over the prior art. If each of the inventions shares the same significant structural element, then it provides the special technical feature which is required to establish unity of invention.

In the present case, genes and their expressed proteins from skin cells have been sequenced. The applicant has provided no evidence that the nucleotide sequences of the present application, and the peptides they express, all form a group of protein types sharing a significant structural element. On the contrary, the putative peptides derived from the nucleotide sequences of the application have a wide range of functions based on their similarity to known proteins. (see Table 2) At best, it appears from Table 2 that there may be 76 distinct protein types which share a common function, and therefore may share a common significant structural element. However, most of the polynucleotides and peptides which do not appear on Table 2, have not have been identified in terms of their function, much less, whether any of them have a shared significant structural element. Therefore, the ISA is unable to confidently determine the number of inventions, on the basis of a shared significant structural element. Thus, at this stage, in the absence of a complete polynucleotide peptide concordance, or the definition of a special technical feature which is common to two or more sequences, this ISA considers that there are 72 groupings of sequences, which encompass the 725 sequences.

While the ISA is unable to determine the precise number of inventions in this application it is prepared, as a service, to search a first group of ten sequences for a single search fee. This offer is provided purely as a service to the applicant and should not be taken as having any bearing on the ISA's assessment of the number of inventions claimed in these 10 sequences. The ISA also agrees to search the two further inventions specified by the applicant in their letter of 30 August 2001, for two additional search fees. As such, the ISA has searched SEQ ID NOS 1-10, 147, 196, 294, 295, 413-5 and 417.